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From: Slobodyansky, Elizabeth
Sent: Tuesday, August 22, 2006 6:23 PM
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Please search for case 10/665,715:

ES

SEQ ID NO: 16 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner
Art Unit 1652
REM 2D83
571-272-0941
MAILBOX 2C70

10-665,715

Searcher: _____

Searcher Phone: _____

Date Searcher Picked up: _____

Date completed: 8-25-06

Searcher Prep Time: _____

Online Time: _____

Type of Search

NA# _____ AA# _____

S/L: _____ Oligomer: _____

Encode/Transl: _____

Structure #: _____ Text: _____

Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____

DIALOG: _____

QUESTEL/ORBIT: _____

LEXIS/NEXIS: _____

SEQUENCE SYSTEM: _____

WWW/Internet: _____

Other (Specify): _____

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Copyright	GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.	Aay83250	F-box pro
OM protein - protein search, using sw model			
Run on:	August 25, 2006, 07:13:17 ; Search time 194 Seconds (without alignments)		
	1277.378 Million cell updates/sec		
Title:	US-10-665-715-16		
Perfect score:	2879		
Sequence:	1 MEPDSVIEDKTIELMCSVPR.....PPSAQNENTRSPSRTTYISR 542		
Scoring table:	BLOSUM62		
	Gap0 10.0 , Gapext 0.5		
Searched:	25899679 seqs, 457216429 residues		
Total number of hits satisfying chosen parameters:	2589679		

ALIGNMENT S.

the total

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	2879	100.0	542	3	AAY956596	Aay96696 Human E3
2	2879	100.0	542	4	AAM79127	Aam79127 Human pro
3	2879	100.0	542	4	AAM40208	Aam40208 Human pol
4	2879	100.0	542	8	ADS88293	Ads88293 Human pro
5	2879	100.0	542	9	AEA01728	Aea01728 Human bet
6	2879	100.0	550	4	AAM41934	Aam41934 Human pol
7	2873	99.8	542	9	ADX05977	Adx05977 Cyclin-de
8	2755.5	95.7	563	8	ADS88282	Ads88282 Human pro
9	2666.5	92.6	529	9	ADX05919	Cyclin-de
10	2661	92.4	508	9	ADX05981	Cyclin-de
11	2458.5	85.4	579	4	AAM78583	Aam78583 Human pro
12	2445.5	84.9	605	4	AAM78582	Aam78582 Human pro
13	2445	84.9	605	8	ADS88274	Ads88274 Human pro
14	2423	84.2	654	4	AAM79568	Aam79568 Human pro
15	2423	84.2	654	4	AAM79567	Aam79567 Human pro
16	2423	84.2	654	4	AAM79566	Aam79566 Human pro
17	2422	84.1	632	4	AAM78584	Aam78584 Human pro
18	2421	84.1	590	4	AAM00847	Aam00847 Human bon
19	2389.5	82.9	608	4	ADM00960	Amd00960 Human bon
20	2384.5	82.8	569	2	AAY24054	Aay24054 Human b
21	2384.5	82.8	569	3	AAY44249	Aay44249 Human cel
22	2384.5	82.8	569	3	ABAB12613	Abab12613 Human bet
23	2384.5	82.9	568	5	AAV05697	Aav05697 Human bet

analysis suggests that deletion of the F-box results in a protein that functions as a dominant negative molecule in vivo. Transient over-expression of delta-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-alpha; I3 can be used to screen for modulators of NF-kappa-B activity. I3 and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections.

Sequence 542 AA:

Query Match 100.0%; Score 2879; DB 3; Length 542;
Best Local Similarity 100.0%; Pred. No. 2, 8e-265;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSDVIETKIELMCSVRSLWLGCAVLESMCALSQPSVRCLQISNGTSSIVS 60	PN WO200157190-A2.
Db	1 MEPSDVIETKIELMCSVRSLWLGCAVLESMCALSQPSVRCLQISNGTSSIVS 60	XX PD 03-AUG-2001.
Qy	61 RKRSEGNYQEKDLCIKYFDQNSDSDQEVFVELISRNCHYOHGHINSYKEMIQLDRFI 120	XX PF 05-FEB-2001; 2001WO-US004098.
Db	61 RKRSEGNYQEKDLCIKYFDQNSDSDQEVFVELISRNCHYOHGHINSYKEMIQLDRFI 120	XX PR 03-FEB-2000; 2000US-00496914.
Qy	121 TALPQQGLDHAENILSYLDARSLLCAEYLCKEMQRVISSEGMLWKKLTERMYRTDPLWKG 180	PR 03-APR-2000; 2000US-00560875.
Db	121 TALPQQGLDHAENILSYLDARSLLCAEYLCKEMQRVISSEGMLWKKLTERMYRTDPLWKG 180	PR 20-JUN-2000; 2000US-00598075.
Qy	181 LSERRGWDQYLFKNRPDTGPPNSFYRSLYPKITDIEETESNRGRHLNQLRQCRSENS 240	PR 19-JUL-2000; 2000US-0062025.
Db	181 LSERRGWDQYLFKNRPDTGPPNSFYRSLYPKITDIEETESNRGRHLNQLRQCRSENS 240	PR 01-SEP-2000; 2000US-00654336.
Qy	241 KGYYCLOYDDEBKIIGLRDNISKIWDKTSLCILKVLTGHTGSVILCLOYDERVTVGSSDS 300	PR 20-OCT-2000; 2000US-00693351.
Db	241 KGYYCLOYDDEBKIIGLRDNISKIWDKTSLCILKVLTGHTGSVILCLOYDERVTVGSSDS 300	PR 30-NOV-2000; 2000US-00728422.
Qy	301 TVRWDVNTEGVNLTLHNEAVHLRFSGNLMTCSKERSIAWDMASATDTLRRVY 360	XX PA (HYSEQ INC.
Db	301 TVRWDVNTEGVNLTLHNEAVHLRFSGNLMTCSKERSIAWDMASATDTLRRVY 360	XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wejhrman T, Goodrich R; DR 2001-476283/51.
Qy	361 GHRAAVNVVDFFDKYIVSAGDRTIKWKSTTCBFRVTLNHKGIACTYQDRDLVWSGS 420	XX DR N-PSDB; AAKS2260.
Db	361 GHRAAVNVVDFFDKYIVSAGDRTIKWKSTTCBFRVTLNHKGIACTYQDRDLVWSGS 420	XX XX Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
Qy	421 SDNTIRLWDIECGACIURVLEGHEELVRCRFDNKRVISAYDGKIKWNLQAALDPRAPA 480	XX XX Claim 20; Page 4147-4148; 6221bp; English.
Db	421 SDNTIRLWDIECGACIURVLEGHEELVRCRFDNKRVISAYDGKIKWNLQAALDPRAPA 480	XX XX The invention relates to polynucleotides (AAKS1456-AAK53435) and the encoded polypeptides (AAM8323-AAM80302) that exhibit activity eliciting to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activation/inhibition activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
Qy	422 STICLRLTVLVEHSGRVRPLQDEFQISSLSSHDFTLWFLNPVPSAQNETRSPSRYYI 540	XX XX Sequence 542 AA;
Db	481 STICLRLTVLVEHSGRVRPLQDEFQISSLSSHDFTLWFLNPVPSAQNETRSPSRYYI 540	XX Query Match 100.0%; Score 2879; DB 4; Length 542;
Qy	541 SR 542	XX Best Local Similarity 100.0%; Pred. No. 2.8e-265;
Db	541 SR 542	XX Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	541 SR 542	XX 1 MEPDPSVBDKTIBMCSVPSRSLWLGCAVLESMCALSQLOMSPSVRCLQISNGTSSIVS 60
Db	541 SR 542	XX 1 MEPDPSVBDKTIBMCSVPSRSLWLGCAVLESMCALSQLOMSPSVRCLQISNGTSSIVS 60
Qy	541 SR 542	XX 61 RKRPSEGNQYQEKDLCIKYFDQNSDSDQEVFVELISRNCHYOHGHINSYKEMIQLDRFI 120
Db	541 SR 542	XX 61 RKRPSEGNQYQEKDLCIKYFDQNSDSDQEVFVELISRNCHYOHGHINSYKEMIQLDRFI 120
Qy	541 SR 542	XX 121 TALPQQGLDHAENILSYLDARSLLCAEYLCKEMQRVISSEGMLWKKLTERMYRTDPLWKG 180
Db	541 SR 542	XX 121 TALPQQGLDHAENILSYLDARSLLCAEYLCKEMQRVISSEGMLWKKLTERMYRTDPLWKG 180
Qy	541 SR 542	XX 181 LSERRGWDQYLFKNRPDTGPPNSFYRSLYPKITDIEETESNRGRHLNQLRQCRSENS 240
Db	541 SR 542	XX 181 LSERRGWDQYLFKNRPDTGPPNSFYRSLYPKITDIEETESNRGRHLNQLRQCRSENS 240
Qy	541 SR 542	XX DE Human protein SEQ ID NO 1789.
Db	541 SR 542	XX XX Human; cytokine; cell proliferation; cell differentiation; haemopoiesis; vaccine; peptide therapy; stem cell growth factor; cancer; arthritis; tissue growth factor; immunomodulatory; gene therapy; gene therapy; nervous system disorder; inflammation.
Qy	541 SR 542	XX OS Homo sapiens.
Db	541 SR 542	XX XX

Qy	361 GHRAAVNVDKDKIVIVSASGDRTIKVWSTSTCEPVRTLNGHKGIACLQYRDLVSGS	420	CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Other uses include the utilisation of the activities such as: Immune system suppression; Activin/inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukemias and C.N.S disorders. Note: The sequence data for this patient did not form part of the printed specification
Db	361 GHRAAVNVDKDKIVIVSASGDRTIKVWSTSTCEPVRTLNGHKGIACLQYRDLVSGS	420	
Qy	421 SDNTIRLWDIBCGACURVLGEELVRCIRFDNKRIVSGAYDGKIKWDLQALDPRPA	480	
Db	421 SDNTIRLWDIBCGACURVLGEELVRCIRFDNKRIVSGAYDGKIKWDLQALDPRPA	480	
Qy	481 STLCIRTLVEHSGRVFRPLQDEFQISSLSSHDDTLWDFLNVPPSAQNETRSPSRYYI	540	
Db	481 STLCIRTLVEHSGRVFRPLQDEFQISSLSSHDDTLWDFLNVPPSAQNETRSPSRYYI	540	
Qy	541 SR 542		Sequence 542 AA;
Db	541 SR 542		Query Match 100.0%; Score 2879; DB 4; Length 542; Best Local Similarity 100.0%; Pred. No. 2.8e-265; Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 3			
ID	AAM40208 standard; protein; 542 AA.		
XX			
AC	AAM40208;		
XX			
DT	22-OCT-2001 (first entry)		
XX			
DE	Human polypeptide SEQ ID NO 3353.		
XX			
KW	Human; nootropic; immunosuppressant; cyrostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000WO-US034263.		
XX			
PR	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552117.		
PR	20-JUN-2000; 2000US-05598042.		
PR	03-AUG-2000; 2000US-00620312.		
PR	14-SEP-2000; 2000US-00653450.		
PR	19-OCT-2000; 2000US-068219.		
PR	29-NOV-2000; 2000US-0069036.		
PR	29-NOV-2000; 2000US-0072734.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich RT, Dumanac RT;		
PI	XX		RESULT 4
XX			ADS88293
DR	WPI; 2001-442253/47.		ID ADS88293 standard; protein; 542 AA.
DR	N-PSDB; AAI61364.		XX
XX			AC ADS88293;
PT	Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.		XX
PT	XX		DT 18-NOV-2004 (first entry)
XX			XX
PS	Example 5; SEQ ID NO 3353; 10078pp; English.		DE Human protein of a TNF-alpha signalling pathway complex Seq 148.
XX			XX
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAI38642-AAI2213) with nootropics, immunosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as		KW protein complex; tumour necrosis factor-alpha signalling pathway; TNF-alpha; chronic inflammatory disease; rheumatoïd arthritis; inflammatory bowel disease; infectious disease; septic shock; bacterial infection; neurological disease; stroke-induced inflammation; neurodegenerative disease; cancer; antiinflammatory; antiarthritic; antirheumatic; cytostatic; antibacterial; gene therapy; human.
CC			

OS Homo sapiens.		Db 301 TVRVWDVNTGEVLNTLHHNEAVLHHRFSNLGMVTSKDRSATIDITLRRVIL 360
XX WO2004035783-A2.	Qy 361 GHRAAVNVDFFDKYIISASGRTIKWSTSTCEVRTLNGHKPGIACLOYFDRLVSGS 420	
XX 29-APR-2004.	Db 361 GHRAAVNVDFFDKYIISASGRTIKWSTSTCEVRTLNGHKRGTAQLODPRAPA 420	
XX 24-SEP-2003; 2003WO-EP050655.	Qy 421 SDNTIRLWDIECGACRVLGEELBVRCAIRFDNKRKIVSGAYDGKIKWDLQALDPRAPA 480	
PF XX 26-SEP-2002; 2002EP-00021805.	Db 421 SDNTIRLWDIECGACRVLGEELBVRCAIRFDNKRKIVSGAYDGKIKWDLQALDPRAPA 480	
PR 10-FEB-2003; 2003EP-00100274.	Qy 481 STLCRLTLEHSGRFLQFDEFQISSLSSHDPTILWDFLNPPSAONETRSPSRITYI 540	
XX (CBLL-) CELLZONE AG.	Db 481 STLCRLTLEHSGRFLQFDEFQISSLSSHDPTILWDFLNPPSAONETRSPSRITYI 540	
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;	Qy 541 SR 542	
XX Superti-Furga G, Kruse U;	Db 541 SR 542	
XX WPI: 2004-348460/32.		
PT New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha/TNF-alpha-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.	RESULT 5 A0A01728 standard; protein; 542 AA. XX DT 14-JUL-2005 (first entry) XX Human beta-transducin repeat containing protein 2. DE XX Beta-transducin repeat containing protein 2; beta-TrCP2; cytosatic; drug screening; antisense therapy; RNA interference; cancer; neoplasm; tumor; metastasis. KW XX Homo sapiens. XX WO2005042701-A2. XX PD 12-MAY-2005. XX PF 19-OCT-2004; 2004WO-US034801. XX PR 21-OCT-2003; 2003US-0513525P. XX PA (UNY) UNIV NEW YORK STATE. XX PI Pagano M; XX DR WPI: 2005-333701/34. XX N-PSDB; AEA01726, AEA01727.	
XX Example: SEQ ID NO 148; 1980pp; English.		
XX This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosis or treating chronic inflammatory diseases such as rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. According, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytosatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway of the invention.		
XX SQ Sequence 542 AA;		
XX Query Match 100.0%; Score 2879; DB 8; Length 542; Best Local Similarity 100.0%; Pred. No. 2.8e-265; Indels 0; Gaps 0; Matches 542; Conservative 0; Mismatches 0;		
Qy 1 MEPDSVIEDKTIELMCSVLSLGCANLYVESMCALSCIQSMPSVRCLQISNGTSSVIVS 60		
Db 1 MEPDSVIEDKTIELMCSVLSLGCANLYVESMCALSCIQSMPSVRCLQISNGTSSVIVS 60		
Qy 61 RKRPSFGNQYKEKDLCIKYFDOWSESDOYEFVHLRSMCHYQHGHSNSYLKPMQLQDRFI 120		
Db 61 RKRPSFGNQYKEKDLCIKYDQWSSDQYEVHHLRSMCHYQHGHSNSYLKPMQLQDRFI 120		
Qy 121 TALPEQGLDHAENILSYLDARSILCAAEELVKEMWORVISSEGMLMKKLTRMVRTDPLWKG 180		
Db 121 TALPEQGLDHAENILSYLDARSILCAAEELVKEMWORVISSEGMLMKKLTRMVRTDPLWKG 180		
Qy 181 LSERRGWDQYLFKNRPDTGPPNSPFLSLPKIQDIETESWNGRHLNQLQCRSENS 240		
Db 181 LSERRGWDQYLFKNRPDTGPPNSPFLSLPKIQDIETESWNGRHLNQLQCRSENS 240		
Qy 241 KGVYCYQDDEKIKIISGLRDNISKWMDKTSLECLKVLTGHGTGSVLCQYDERTVTGSSS 300		
Db 241 KGVYCYQDDEKIKIISGLRDNISKWMDKTSLECLKVLTGHGTGSVLCQYDERTVTGSSS 300		
Qy 301 TVRVWDVNTGEVLNTLHHNEAVLHHRFSNLGMVTSKDRSATIDITLRRVIL 360		

CC short interfering RNA (siRNA) molecule. A method of reducing Cdc25A
 CC degradation in a cell involves reducing beta-TrCP1 and/or TrCP2 in the cell e.g. by administering
 CC the amount of beta-TrCP1 and/or TrCP2 in the cell. The methods, inhibitors, agents, and
 CC antisense or siRNA molecule. The methods, inhibitors, agents, and
 CC compositions of the invention are useful for treating cancers, including
 CC metastatic and primary cancers, and cancers characterized by solid or non-
 CC -solid tumors.

SQ Sequence 542 AA;

Query Match 100.0%; Score 2879; DB 9; Length 542;
 Best Local Similarity 100.0%; Pred. No. 2.8e-265;
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSVIEDKTIELMCSPVSPRSILWLGANLYVESMCALSCLOSMPSTYRCLOISNGTSSVIYS 60

Db 1 MEPSVIEDKTIELMCSPVSPRSILWLGANLYVESMCALSCLOSMPSTYRCLOISNGTSSVIYS 60

Qy 61 RKRPEGNYQKEKDLCIYKPDQWSSESDQVFVEHLSRSMCHYQHGHSNLYLKPMQLQRDFI 120

Db 61 RKRPEGNYQKEKDLCIYKPDQWSSESDQVFVEHLSRSMCHYQHGHSNLYLKPMQLQRDFI 120

Qy 121 TALPQGLDHAENLISYLDARSCLAAELVCKEWORVISGMLWKLLIERNMRVDPLWKG 180

Db 121 TALPQGLDHAENLISYLDARSCLAAELVCKEWORVISGMLWKLLIERNMRVDPLWKG 180

Qy 181 LSRERGMWDQYLFKNRPRTDGPNFSYRSLYKPIKLIQDIETESNWRGRHNLQRIQCRSENS 240

Db 181 LSRERGMWDQYLFKNRPRTDGPNFSYRSLYKPIKLIQDIETESNWRGRHNLQRIQCRSENS 240

Qy 241 KGVVYCYQQDDEKEIISGLRDNISKIKWDTSLECLKVLTGHTGSVLCLQYDERIVTGSSDS 300

Db 241 KGVVYCYQQDDEKEIISGLRDNISKIKWDTSLECLKVLTGHTGSVLCLQYDERIVTGSSDS 300

Qy 301 TVRVWDVNTRGEVLNTLIIHNEAVHLRFSNGLMVTCSKDRSIAWDMASATDTIIRRVLV 360

Db 301 TVRVWDVNTRGEVLNTLIIHNEAVHLRFSNGLMVTCSKDRSIAWDMASATDTIIRRVLV 360

Qy 361 GHRAAVNVYDDDKYTIVASAGDRTIKVWSTSTCEFVRTLNGHKGRIACILOYDRDLUVSGS 420

Db 361 GHRAAVNVYDDDKYTIVASAGDRTIKVWSTSTCEFVRTLNGHKGRIACILOYDRDLUVSGS 420

Qy 421 SDNTNTRLWDIECGACIYRLVSGHEELYRCITFDNKRKIVSGAYDGKIKWDLQAALDPRADA 480

Db 421 SDNTNTRLWDIECGACIYRLVSGHEELYRCITFDNKRKIVSGAYDGKIKWDLQAALDPRADA 480

Qy 481 STLCIRTLVEHSGRYFRVLQDEFOLISSHDFTLNVPPSAQNTRSPSTYTYI 540

Db 481 STLCIRTLVEHSGRYFRVLQDEFOLISSHDFTLNVPPSAQNTRSPSTYTYI 540

Qy 541 SR 542

Db 541 SR 542

Qy RESULT 6

AAM41994 standard; protein; 550 AA.

XX DE Human polypeptide SEQ ID NO 6925.

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

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XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

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XX AC AAM41994;

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XX AC AAM41994;

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XX DE Human polypeptide SEQ ID NO 6925.

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XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

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XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 6925.

XX AC AAM41994;

XX DT 22-OCT-2001 (first entry)

PF 24-SEP-2003 ; 2003WO-EP050655 .	Qy 400 NGHKRGIAQIACQYRDRLLWVGSQSDNTIRLWDIEGCACLRLEGHEELVRCIREDFDNKRIVSG 459
XX	Db 421 NGHKRGIAQIACQYRDRLLWVGSQSDNTIRLWDIEGCACLRLEGHEELVRCIREDFDNKRIVSG 480
PR 26-SEP-2002 ; 2002EP-00021809 .	
PR 10-FEB-2003 ; 2003BP-00100274 .	
XX (CELL-) CELLZONE AG .	Qy 460 AYDGKIKWDLQDAPASTLCLRTLVHESGRVFLQFDEQIISSSHDDTLLINDF 519
XX	Db 481 AYDGKIKWDLQDAPASTLCLRTLVHESGRVFLQFDEQIISSSHDDTLLINDF 540
PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Ruester B;	Qy 520 LNVPDAQNETHSPRSRTYYISR 542
PI Superti-Purga G, Kruse U;	Db 541 LNVPDAQNETHSPRSRTYYISR 563
XX	
DR WPI : 2004-348460/32 .	
XX	
PT New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.	RESULT 9 ADX05979 ID ADX05979 standard; protein; 529 AA .
XX	XX
PS Example: SEQ ID NO 137; 1980pp; English .	AC ADX05979 ;
XX	XX
CC This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosis, or treating chronic inflammatory diseases such as rheumatoid arthritis and inflammatory bowel disease; infectious diseases such as septic shock and bacterial infections; neurological diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antiinflammatory, antiarthritic, antirheumatic, cytostatic, and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification to form novel complexes of the TNF-alpha signalling pathway	DT 21-APR-2005 (first entry) DE Cyclin-dependent kinase modulation biomarker SEQ ID NO 544 . XX KW cytostatic; cyclin-dependent kinase; cdk; biomarker . XX OS Homo sapiens . XX PN WO2005012875-A2 . XX PD 10-FEB-2005 . XX PF 29-JUL-2004 ; 2004WO-US024424 . XX PR 29-JUL-2003 ; 2003US-0490890P . XX PA (BRIM) BRISTOL-MYERS SQUIBB CO . XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW; XX DR WPI-2005-163068/17 . XX N-PSDB; ADX05978 .
XX	
PS Example: SEQ ID NO 137; 1980pp; English .	XX
XX	
CC This invention describes a novel method of predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.	Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-dependent kinase activity.
XX	Claim 5; SEQ ID NO 544; 141pp; English .
PS	PT PT PT
XX	CC CC CC
CC This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized generic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-[5-[(1,1-Dimethylethyl)-2-(oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/obtained pct sequences. This sequence represents a biomarker used in the method of the invention.	CC CC CC
XX	CC CC CC
PS Sequence 563 AA;	CC CC CC
Qy Query Match 95.7%; Score 2755.5; DB 8; Length 563;	CC CC CC
Best Local Similarity 93.3%; Pred. No. 1..8e-253; Indels 21; Gaps 1;	CC CC CC
Matches 525; Conservative 2; Mismatches 15;	CC CC CC
Db 1 MEPSVIEKTIELMCSVRSLWLGANLVSMCALSCQMSVRCL-----48	CC CC CC
Qy 49 -----QISNGTSSV1SRKPSSEGNYQKEKDLCIXFDOMSEDOVEFVHLIRM 99	CC CC CC
Db 61 ESPKKSALQISNGTSSV1SRKPSSEGNYQKEKDLCIXFDOMSEDOVEFVHLIRM 120	CC CC CC
Qy 100 CHYQGHINNSYLKPMQLQRFITALPEQGLDHIAENILSTYLDARSCLCAELVKEWORYS 159	CC CC CC
Db 121 CHYQGHINNSYLKPMQLQRFITALPEQGLDHIAENILSTYLDARSCLCAELVKEWORYS 180	CC CC CC
Qy 160 EGMLWKKLTERMVTDPLWKGLSERRGWQYLFKNRPTGPPNSFYRSVSYKTIQDITI 219	CC CC CC
Db 181 EGMLWKKLTERMVTDPLWKGLSERRGWQYLFKNRPTGPPNSFYRSVSYKTIQDITI 240	CC CC CC
Qy 220 ESNWRCGRNHLQR1QCRSENSKGYCYCLODDEKL1SGLRDNS1KIWDDKTSLECLVKLTH 279	CC CC CC
Db 241 ESNWRCGRNHLQR1QCRSENSKGYCYCLODDEKL1SGLRDNS1KIWDDKTSLECLVKLTH 300	CC CC CC
Qy 280 TGSVLCLQYDERTVGTGSSDSTVRYDWNTGEVENTLIIHNEAVUHLRFSGNLMVTCSD 339	CC CC CC
Db 301 TGSVLCLQYDERTVGTGSSDSTVRYDWNTGEVENTLIIHNEAVUHLRFSGNLMVTCSD 360	CC CC CC
Qy 340 RSIAWMDMASATDTLRRVLUVGRRAAVNTVDFDDKYIVSASGDTIKWSTSTCEFVTL 399	CC CC CC
Db 361 RSIAWMDMASATDTLRRVLUVGRRAAVNTVDFDDKYIVSASGDTIKWSTSTCEFVTL 420	CC CC CC
Query Match 92.6%; Score 2666.5; DB 9;	XX
Best Local Similarity 92.4%; Pred. No. 5.2e-245;	
Matches 512; Conservative 1; Mismatches 4;	
Indels 37; Gaps 3;	

				PRSLWLGCAANLVESMCALSCQNSPVRCL
1	MEDPSIEDKTELM-CSV	- - - - -	- - - - -	1
Qy				
Db				
1	MEDPSIEDKTELM-CSV	- - - - -	- - - - -	35
1	MEDPSIEDKTELM-CLMNTSVMEDQNEDESPKKNL-	- - - - -	- - - - -	
Qy				
Db				
49	QISNGTSSVIVSRKRPESEGYOKEDLCIYKFDMSESDOVEFYEHLISRMCYHQGH1N	108		
36	QISNGTSSVIVSRKRPESEGYOKEDLCIYKFDMSESDOVEFYEHLISRMCYHQGH1N	95		
109	SYLKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWORVISEGMLWKKLI	168		
96	SYLKPMQLQDFITALPEQGLDHIENILSYLDARSILCAELVCKEWORVISEGMLWKKLI	155		
169	ERMRVRTDPLWKGLSBERGDWYLFKNRPTDGPPNSYRSLPKIQLODIETIESWRGRH	288		
156	ERMRVRTDPLWKGLSSERGDWYLFKNRPTDGPPNSYRSLPKIQLODIETIESWRGRH	215		
229	NLQRIOCRSENSKGYVCLQYDKEKLISGLRDNSKIKWDKTSLECKLKVLTGHTGSVLCLQY	288		
216	NLQRIOCRSENSKGYVCLQYDKEKLISGLRNSKIKWDKTSLECKLKVLTGHTGSVLCLQY	275		
289	DERVIVTGSSDSTVRWDVNTGEVNTLIIHNEAVHLRFNSNGLMVTCSDRSIAWDNA	348		
276	DERVIVTGSSDSTVRWDVNTGEVNTLIIHNEAVHLRFNSNGLMVTCSDRSIAWDNA	335		
349	SATDITLRRLVGHRAVNVDFFDKYIVSASGDRTIKWSNSTCEFVRTLNGKRGIAIC	408		
336	SATDITLRRLVGHRAVNVDFFDKYIVSASGDRTIKWSNSTCEFVRTLNGKRGIAIC	393		
409	LQYDRLLVGSQSDNTIRLWDTEGACRVLLEGHEBLVRCIRFDNKRIIVSGAYDKIKW	465		
396	LQYDRLLVGSQSDNTIRLWDIEGCAVLRLLEGHEBLVRCIRFDNKRIIVSGAYDKIKW	455		
469	DIAQALDPRAPASTCLCLRIVEHSGRVFLQDEFOTISSSHDTLWDFLNTPPSAQN	528		
456	DIAQALDPRAPASTCLCLRIVEHSGRVFLQDEFOTISSSHDTLWDFLNTPPSAQN	515		
529	EPRSPSRYTYISR	542		
516	EPRSPSRYTYISR	529		

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RESULT 10
ADX05981 standard; protein; 508 AA.
ID ADX05981
XX
AC AC05981;
DT 21-APR-2005 (First entry)
XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 546.
DE XX
XX cytostatic; cyclin-dependent kinase; cdk; biomarker.
KW XX
OS Homo sapiens.
XX PN WO2005012875-A2.
XX
XX PD 10-FEB-2005.
XX PF 29-JUL-2004; 2004WO-US024424.
XX PR 29-JUL-2003; 2003US-0490890P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX WPI: 2005-161068/17.
DR N-PSDB; ADX05980.
XX PT Biomarkers useful for predicting or determining the response
PT to a cancer treatment comprising administration of a modula-

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ID	AAM78533	standard; protein;	579 AA.
AC			
XX			
XX			
XX	06-NOV-2001	(First entry)	
DE	Human Protein SEQ ID NO 1245.		
XX	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemato poesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.		
XX	OS	Homo sapiens.	
XX	WO200157190-A2.		
XX	PD	09-AUG-2001.	
XX	PF	05-FEB-2001; 2001WO-US004098.	
XX	PR	03-FEB-2000; 2000US-00496914.	
PR	27-APR-2000; 2000US-00560875.		
PR	20-JUN-2000; 2000US-00598075.		
PR	19-JUL-2000; 2000US-00620345.		
PR	01-SEP-2000; 2000US-00654936.		
PR	15-SEP-2000; 2000US-00663561.		
PR	20-OCT-2000; 2000US-00693345.		
PR	30-NOV-2000; 2000US-00728432.		
XX	PR	(HYSE-) HYSEQ INC.	
XX	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
XX	WPI; 2001-476283/51.		
DR	N-PSDB; AAK1716.		
PT	Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.		
PT	Claim 20; Page 3504-3505; 6221pp; English.		
XX	The invention relates to polynucleotides (AAK51456 AAK53435) and the encoded polypeptides (AAM78533-AAMB0102) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The CC polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemato poiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication		
XX	Sequence 579 AA;		
Query Match	85.4%	Score 2458.5; DB 4; Length 579;	
Best Local Similarity	79.1%	Prod. No. 4.3e-225;	
Matches 458; Conservative 49; Mismatches 35; Indels 37; Gaps 4;			
PA	1 MEP-DSV1EDKTIELMCSVPRSIWLGCANLVESMCALSC-----39		
PA	1 MDPAEAV1QEKALKFMCMSMPRSIWLGCSSSLADSMPSLRCLYNPGTGAATQFTYNSCARL 60		
DB	40 -----QEMPAEV1QEKALKFMCMSMPRSIWLGCSSSLADSMPSLRCLYNPGTGAATQFTYNSCARL 60		
Qy	61 CLNQETVCLASTAMKTENCVAKTKLANGTSSM1VKQKLSSAYERKEKLVCKYFPEWSE 120		
Qy	SDQVEFWHELLSQMCHYQHGHINSYKPLMLORDFTALPARGLDHAENILSYLDAKSLC 145		
DB	121 SDQVEFWHELLSQMCHYQHGHINSYKPLMLORDFTALPARGLDHAENILSYLDAKSLC 180		
Qy	146 AAELVCKEWYRVIQSEGMLWKKLIERMYRTDPLWKGLSERRGMDQYDDEKEK1ISGLRDNSIK 263		
DB	181 AAELVCKEWYRVIQSEGMLWKKLIERMYRTDPLWKGLSERRGMDQYDDEKEK1ISGLRDNSIK 240		
Qy	204 FYRLSPKIIQDIEITESNWICGRHLNQLQRCRSENSKGVYCLQYDDEKEK1ISGLRDNSIK 263		
DB	241 FYRALPKIIQDIEITESNWICGRHLNQLQRCRSENSKGVYCLQYDDEKEK1ISGLRDNSIK 300		
Qy	264 IWDKTSLECLCKVLTLGHGTGSVILCQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 323		
DB	301 IWDKNTLECKRLTLGHGTGSVILCQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 360		
Qy	324 LHLRFNSGLMYTCISKDORSIAWTDMASTADTILRRLVGHRAVNYYDFDDKYIVASGDR 383		
DB	361 LHLRFNSGLMYTCISKDORSIAWTDMASTADTILRRLVGHRAVNYYDFDDKYIVASGDR 420		
Qy	384 TIKWSTSTCEFVRLNGHKG1CQYRDLVVSSESDNTIRLWDIEGAGLRLVLEGHE 443		
DB	421 TIKWNTSTCEFVRLNGHKG1CQYRDLVVSSESDNTIRLWDIEGAGLRLVLEGHE 480		
Qy	444 ELVRIC1REDKNKRIVSGAYDGKIKWVLDQALDPRAPSTLCLRTLYEHSGRVFR1QDEF 503		
DB	481 ELVRIC1RFDNKRIVSGAYDGKIKWVLDQALDPRAPSTLCLRTLYEHSGRVFR1QDEF 540		
Qy	504 QIISSSHDDTILWDLNVPPSAQNERTSPSRTYIISR 542		
DB	541 QIVSSSSHDDTILWDLNDPAQAQPSPRTYIISR 579		
	RESULT 12 AAM78582		
	ID AAM78582 standard; protein; 605 AA.		
	XX AAM78582;		
	AC		
	XX DT 06-NOV-2001 (first entry)		
	XX DE Human protein SEQ ID NO 1244.		
	XX KW Human; cytokine; cell proliferation, cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemato poiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.		
	XX KW Homo sapiens.		
	XX XX WO200157190-A2.		
	XX PN WO200157190-A2.		
	XX PD 09-AUG-2001.		
	XX PF 05-FEB-2001; 2001WO-US004098.		
	XX PR 03-FEB-2000; 2000US-00496914.		
	PR 27-APR-2000; 2000US-00560875.		
	PR 20-JUN-2000; 2000US-00598075.		
	PR 19-JUL-2000; 2000US-00620345.		
	PR 01-SEP-2000; 2000US-00654936.		
	PR 15-SEP-2000; 2000US-00663561.		
	PR 20-OCT-2000; 2000US-00693345.		
	PR 30-NOV-2000; 2000US-00728432.		
	(HYSE-) HYSEQ INC.		
	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
	WPI; 2001-476283/51.		
	DR N-PSDB; AAK1716.		
	PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.		
	PT Claim 20; Page 3504-3505; 6221pp; English.		
	CC The invention relates to polynucleotides (AAK51456 AAK53435) and the encoded polypeptides (AAM78533-AAMB0102) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The CC polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, CC e.g. stem cell growth factor activity, haemato poiesis regulating CC activity, tissue growth factor activity, immunomodulatory activity and CC activity/inhibin activity and may be useful in the diagnosis and/or CC treatment of cancer, leukaemia, nervous system disorders, arthritis and CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the CC sequence listing were missing at the time of publication		
	XX Sequence 579 AA;		
	Query Match 85.4% Score 2458.5; DB 4; Length 579;		
	Best Local Similarity 79.1% Prod. No. 4.3e-225;		
	Matches 458; Conservative 49; Mismatches 35; Indels 37; Gaps 4;		
	PA 1 MEP-DSV1EDKTIELMCSVPRSIWLGCANLVESMCALSC-----39		
	PA 1 MDPAEAV1QEKALKFMCMSMPRSIWLGCSSSLADSMPSLRCLYNPGTGAATQFTYNSCARL 60		
	DB 40 -----QEMPAEV1QEKALKFMCMSMPRSIWLGCSSSLADSMPSLRCLYNPGTGAATQFTYNSCARL 60		
	Qy 61 CLNQETVCLASTAMKTENCVAKTKLANGTSSM1VKQKLSSAYERKEKLVCKYFPEWSE 120		
	Qy SDQVEFWHELLSQMCHYQHGHINSYKPLMLORDFTALPARGLDHAENILSYLDAKSLC 145		
	DB 121 SDQVEFWHELLSQMCHYQHGHINSYKPLMLORDFTALPARGLDHAENILSYLDAKSLC 180		
	Qy 146 AAELVCKEWYRVIQSEGMLWKKLIERMYRTDPLWKGLSERRGMDQYDDEKEK1ISGLRDNSIK 263		
	DB 181 AAELVCKEWYRVIQSEGMLWKKLIERMYRTDPLWKGLSERRGMDQYDDEKEK1ISGLRDNSIK 240		
	Qy 204 FYRLSPKIIQDIEITESNWICGRHLNQLQRCRSENSKGVYCLQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 323		
	DB 241 FYRALPKIIQDIEITESNWICGRHLNQLQRCRSENSKGVYCLQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 360		
	Qy 264 IWDKTSLECLCKVLTLGHGTGSVILCQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 383		
	DB 301 IWDKNTLECKRLTLGHGTGSVILCQYDDEVTRIVGSDSTVRYWDVNTGEVNTLILHNEAV 443		
	Qy 324 LHLRFNSGLMYTCISKDORSIAWTDMASTADTILRRLVGHRAVNYYDFDDKYIVASGDR 480		
	DB 361 LHLRFNSGLMYTCISKDORSIAWTDMASTADTILRRLVGHRAVNYYDFDDKYIVASGDR 540		
	Qy 384 TIKWSTSTCEFVRLNGHKG1CQYRDLVVSSESDNTIRLWDIEGAGLRLVLEGHE 579		
	DB 421 TIKWNTSTCEFVRLNGHKG1CQYRDLVVSSESDNTIRLWDIEGAGLRLVLEGHE 614		
	Qy 444 ELVRIC1REDKNKRIVSGAYDGKIKWVLDQALDPRAPSTLCLRTLYEHSGRVFR1QDEF 503		
	DB 481 ELVRIC1RFDNKRIVSGAYDGKIKWVLDQALDPRAPSTLCLRTLYEHSGRVFR1QDEF 540		
	Qy 504 QIISSSHDDTILWDLNVPPSAQNERTSPSRTYIISR 542		
	DB 541 QIVSSSSHDDTILWDLNDPAQAQPSPRTYIISR 579		
	RESULT 12 AAM78582		
	ID AAM78582 standard; protein; 605 AA.		
	XX AC		
	XX XX DT 06-NOV-2001 (first entry)		
	XX XX PR 03-FEB-2000; 2000US-00496914.		
	PR 27-APR-2000; 2000US-00560875.		
	PR 20-JUN-2000; 2000US-00598075.		
	PR 20-OCT-2000; 2000US-00620325.		
	PR 01-SEP-2000; 2000US-00654936.		
	PR 15-SEP-2000; 2000US-00663561.		
	PR 20-NOV-2000; 2000US-00693325.		
	PR 30-NOV-2000; 2000US-00728422.		
	(HYSE-) HYSEQ INC.		
	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
	WPI; 2001-476283/51.		
	DR N-PSDB; AAK51715.		

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 3503-3504; 6221pp; English.
 XX
 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM80123-AAM80102) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 4; Length 605;

Best Local Similarity 75.7%; Pred. No. 8e-224;

Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

SQ Query 1 MEP-DSVIEDKTIBLMCSVPRSLWLGCAANLVESEMCAISCL----- 39

Dbb 1 MDPAEAVLQEQKALKFPMCSVPRSLWLGCSLADSMPSLRCLYDQFQAFMNSSEREDC 60

Qy Qy 40 -----OSMPSPVRCL---QISNGTSSVIV 59

Dbb 61 NNGEPPRKLIPEPKNSLRLQTYNTNSCARLCLNQETVCLASTAMKCENVAKTKLNGTSSVM 120

Qy 60 SRRKRSEGVNQYKEKDLCIYTFDOWSESDOVEFVHLISRMCYQOHGHINSYLKPMLORD 119

Dbb 121 PKQRKLSSAYEKERFLCVYKPEQNSESDQVEFVHLISRMCYQOHGHINSYLKPMLORD 180

Qy 120 ITALPEOGDHIAENILSYLDARSILCAARFLVKEWORYTSEGMLWKLLIERNVYRTDPLWK 179

Dbb 181 ITALPARGGDHIAENILSYLDARSILCAARFLVKEWORYTSDGMWKLLIERNVYRTDLSWR 240

Qy 180 GLSERRGWQYQLFKNPRTG- PPNSFVYSLYPKIIQDETEISNWRCGRHNLQRIQCRS 237

Dbb 241 GLAERRGWCQYLFKNPKPPGNAPPNSFVALYPKIIQDETEISNWRCGRHSLQRIQCRS 300

Qy 238 ENSKGVYCVQYDDERIKISGIRDNSIJKIWKNTLSCLEKVLTGFGSVLCLQYDERTVITGS 297

Dbb 301 ETSKGVYCVQYDDKIVSGIRDNTIKIWKNTLCEKVLITGHTGSVCLQYDERTVITGS 360

Qy 298 SDSTPVRWQYDNTGEVLTNTLJHHNEAVLHLRFNSLGMVTCSKDRSIAVMDMASATDITLRR 357

Dbb 361 SDSTPVRWQYDNTGEMLNNTLTHCPDAVLHRENNNMVTSKDRSIAVMDMASPTDITLRR 420

Qy 358 VLVGHRAAAANVVDPPDKYVSAASGDRITKWNSTCTCEFRTLIGHKRGIAQLYDRDLVY 417

Dbb 421 VLVGHRAAAANVVDPPDKYVSAASGDRITKWNSTCTCEFRTLIGHKRGIAQLYDRDLVY 480

Qy 418 SGSSDNTIRLWDIEGACIYRLEGEELVRCIRFDNKRVGAYDGVKWDIQAALDPR 477

Dbb 481 SGSSDNTIRLWDIEGACIYRLEGEELVRCIRFDNKRVGAYDGVKWDIQAALDPR 540

Qy 478 APASTLICRVTLVENSGRVRPLQFDEFQISSLSSHDITLWDFUNVPPSAQNTRSPSRVY 537

Dbb 541 APAGTFLCLRTLVENSGRVRPLQFDEFQIVSSSHDDTILWDFLNDPAAOAEPPRSRSRY 600

Qy 538 TYISR 542

Dbb 601 TYISR 605

RESULT 13

ADS88274 standard; protein; 605 AA.

ID ADS88274

XX

SQ Sequence 605 AA;

Query Match 84.9%; Score 2445.5; DB 8; Length 605;

Best Local Similarity 75.7%; Pred. No. 8e-224;

Matches 458; Conservative 49; Mismatches 35; Indels 63; Gaps 4;

Dbb 1 MEP-DSVIEDKTIBLMCSVPRSLWLGCAANLVESEMCAISCL----- 39

Qy 40 -----OSMPSPVRCL---QISNGTSSVIV 59

Dbb 61 NNGEPPRKLIPEPKNSLRLQTYNTNSCARLCLNQETVCLASTAMKCENVAKTKLNGTSSVM 120

Qy 60 SKRPSEGGNYQEKEKOLCITYFDQNSSEDOVEFVHLISRMCHYQHGHINSYLKPMQLQRDF 119
 Db 121 PKQRKLUSASBKEKLCVCFYFEQMSLCAELVCKEVRVSISEGMLWKKLIERMVRTDPLMK 180
 Qy 120 ITALPEQGLDHIAENILSILDARSPLCAELVCKEVRVSISEGMLWKKLIERMVRTDPLMK 179
 Db 181 ITALPARGLHDIAENILSILDAKSLCAELVCKEVRVTSQGMWLKKLIERMVRTDLSMR 240
 Qy 180 GLSERGRWMQYLPKRNQRTDG - PPNFSFYRSLYPKTQIQTETIESNWRGHRNLIQCRS 237
 Db 241 GLAERGRGWOYLFKNRPDKDNAPPNSFYRALYPKTIQDTEIESNWRGRHSLSRHCs 300
 Qy 238 ENSKGVYCLOYDDEKITSGIRDNSKIKWMTKSLECLKVLIGHTSVLCLQYDERTVITGS 297
 Db 301 ETSKGVYCLOYDQKIVSGRDNTKIKWMTKLNLKRLTQIQLIGHTSVLCLQYDERTVITGS 360
 Qy 298 SDSTRVWDNTGEVLTNLTHNEAVLHLRFSGNLMVTCSDRSIAVMMASATDITLR 357
 Db 361 SDSTRVWDNTGENMLNTLTHCEAVLHLRFNGMMVTCSDRSIAVMMASPTDITLR 420
 Qy 358 VLVGHRAAVNVVDFFDKYIVSASGRTIKWSTSTCEFYRTLNGHKRGIACLQYDRLVY 417
 Db 421 VLVGHRAAVNVVDFFDKYIVSASGRTIKWNTSICEFYRTLNGHKRGIACLQYDRLVY 480
 Qy 418 SGSSDNTNTLWIDIEGACRVLGEHEELVCRIFPDNKRVIVSGAYDGKIKWMDQAAALDR 477
 Db 481 SGSSDNTNTLWIDIEGACRVLGEHEELVCRIFPDNKRVIVSGAYDGKIKWMDLVAALDR 540
 Qy 478 A APASTLCLRTLVEHSGRFLQFDEFQI FISSHHDDTILWDFLNPSPSONETRSPSRVY 537
 Db 541 APAGTLCLRTLVEHSGRFLQFDEFQI VSSSHDDTILWDFLNPDAQAEPPRSPSRVY 600
 Qy 538 TYISR 542
 Db 601 TYISR 605

RESULT 14
 AAM79568 standard; protein; 654 AA.
 ID AAM79568;
 AC AAM79568;
 DT 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 3214.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;
 tissue growth factor; immunomodulatory; cancer; leukaemia;
 nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 OS WO200157190-A2.
 PN 09-AUG-2001.
 PD XX
 PF 05-FBB-2001; 2001WO-US004098.
 PR 03-FBB-2000; 2000US-00496914.
 PR 27-AFR-2000; 2000US-00569875.
 PR 20-JUN-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00651936.
 PR 20-OCT-2000; 2000US-00633561.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSEQ -) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Weijhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR N-PSDB; AAK52701.
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 286-287; 622IPP; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53415) and the
 encoded polypeptides (AM78323-AM80302) that exhibit activity relating to
 cytokine, cell proliferation or cell differentiation or which may induce
 production of other cytokines in other cell populations. The polynucleotides or
 polypeptides are useful in gene therapy, vaccines or
 peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haemopoiesis regulating
 activity, tissue growth factor activity, immunomodulatory activity and/or
 activity/inhibit activity and may be useful in the diagnosis and/or
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation. Note: Records for SEQ ID NO 2110 (AAK52581),
 (AAK52582) and 3656 (AM80020) are omitted as the relevant pages from the
 sequence listing were missing at the time of publication.
 CC
 SQ Sequence 654 AA;
 Query Match 84.12%; Score 2423; DB 4; Length 654;
 Best Local Similarity 72.5%; Pred. No. 1.3e-221;
 Matches 450; Conservative 49; Mismatches 35; Indels 90; Gaps 5;
 CC
 Qy 1 MEP-DSDIEDKTBLM-----
 Db 23 MDPAAVLOQPKALKMMEFRSWCPCQWNTMARSRLATATSTSRVQCSMPRSIWLGESLADS 82
 Qy 33 MCALSC1-----
 Db 83 MPSLRCLYNPGTGAATAQNSSERDCNNGEPPRKIIPEKNSRPSBNQYKEKDLCITYKFQDQWSESDQVQEFV 202
 Qy 40 ----OSMPSYRCL --QISNGTSSVTVSSXRPSBNQYKEKELCYKFQDQWSESDQVQEFV 202
 Db 143 CLASTAMTKTENCVAKTKLNGTSSMIVPKQRLKLSAYKEKELCYKFQDQWSESDQVQEFV 92
 Qy 93 EHLISRMCHYQHGHINSYLPKMLQDFITALPEQGDHTAENILSYLDARSICAEVLCK 152
 Db 203 EHLISQMCHYQHGHINSYLPKMLQDFITALPAQDHTAENILSYLDARSICAEVLCK 262
 Qy 153 EWQRISEGMLWKKLIERMVTDLWKGLSERRGMDQYLFKNRPTDG- PPNSFYSRSLYP 210
 Db 263 EWYRVSQDMWLKKLIERMVTDLWKGLSERRGMDQYLFKNRPTDG- PPNSFYSRSLYP 322
 Qy 211 KIIQDIEITESNWRCRGRHLQRIOQRSSENKSKGVYCLQYDDEKTLISGLRDNISKIWKDTSL 270
 Db 323 KIIQDIEITESNWRCRGRHLQRIOQRSSENKSKGVYCLQYDQKIVSGLRNTIKWKNTL 382
 Qy 271 ECLXWVLTGHTGSGVSLQYDERTVITGSSDSTVRYDWNTGEVLTNLHINEAVLHLRFSN 330
 Db 383 ECKRLTGHTGSGVSLQYDERTVITGSSDSTVRYDWNTGEMLNLHICCAVLHLRFNN 442
 Qy 331 GLMYTCSKDSRISAWVPPSAQNETRSPSHTTY1SR 590
 Db 443 GMMYTCSKDSRISAWVPPSAQNETRSPSHTTY1SR 502
 Qy 391 STCEFVRTLNGHKRGIAQYDRVIAVSSSDNTNTRLWIECGAQLRVEGHEELVRCIR 450
 Db 503 STCEFVRTLNGHKRGIAQYDRVIAVSSSDNTNTRLWIECGAQLRVEGHEELVRCIR 562
 Qy 451 FDNKRIIVSGAYDGKIKWMDQALPAPSTLCLRTLYEHSGRFRLOFDEFQISSH 510
 Db 563 FDNKRIIVSGAYDGKIKWMDQALPAPSTLCLRTLYEHSGRFRLOFDEFQISSH 622
 Qy 511 DDTLWIWDFLNVPSPSAQNETRSPSHTTY1SR 542
 Db 623 DDTLWIWDFLNDPAAQSEPERSPSPSHTTY1SR 654

A;Reference number:	225046
A;Accession:	T50211
A;Status:	Preliminary; translated from GB/EMBL/DBJ
A;Molecule type:	DNA
A;Residues:	1-506 <MCD>
A;Cross-references:	UNIPROT:Q09855; UNIPARC:UPI0000131DC4; EMBL:AL136538; PIDN:C
A;Experimental source:	strain 972h(-); cosmid c30
C;Genetics:	
A;Gene:	SPAC29E6.01; SPDB:SPAC30.05
A;Map position:	1
A;Introns:	43/1; 74/3
RESULT 2	
T16607	
Db	454 DGKIKWDLVAAUDPRAAGTCLRLTLEVEHSGRFLQDFEFQIVSSHDOTLWDFLN 513
Qy	522 VP 523
Db	514 DP 515
Db	514 DP 515
Query Match	23.7%; Score: 683.5 ; DB: 2; Length: 506;
Best Local Similarity	31.3%; Pred. No. 6..1e-44;
Matches	155; Mismatches 147; Indels 95; Gaps 14;
Qy	85 ESDQVEFVEHLISRMCHYQGHINSYLKEMLQRDFITALPEQGLDHAIENILSYLDARS 144
Db	38 ENRIDLIRDLLASLSKEGVVAYNHVRSLLFDTFTEVPEE---VSRLRVFSYLDQLDL 93
Qy	145 CAAELVCKEWORVISEGMLWKKLTERMYRTDPLWKG-----LSBRGW----- 187
Db	94 CKCKLMSKRKWLLEDPGTWKALY-----MOKGWFVNENVLNEFEAMRRTHKFQPQR 145
Qy	188 -----DQVLFKNRPTDGPENSFRSLYPKIQLDIETESWRGR 227
Db	146 FENFLKQONIIGPGYTMELPQOQIF-----DSNRGRJLNNWVY---KEHAHDSLWHRG 198
Qy	228 -----HNLRQIQCSENS----KGVYCLQYDDEKISGLRDNSIKIWDKTSLECLKVLT 277
Db	199 FLYSTFNPNSSIRFAQDFERATLDSVYCVQYDDIMVSSESKDRTVSWVDNSRSFLYLYKLY 258
Qy	82 QWSSEDOVEFVEHLISRMCHYQGHINSYLKEMLQRDFITALPEQGLDHAIENILSYDA 141
Db	82 RWEHEBOLDMDKIVHRLSHKOLGKVDFNFIPELQRDFISNLPA---HVLILFNVNS 137
Qy	142 FSLCAAEVCKEWORVISEGMLWKKLTERMYRTDPLWKGLSERGRGNDQYLPQNRPPTDPGP-
Db	138 DSLSKSCBEVTSWRCAALRGQHMKLIEKNTRSDSLWGLSERKNDLTSRDMSVRR 197
Qy	201 -----PNSFPRSLYPKIQLDIEETENWRGRHNLORIQCSEN 239
Db	198 ICEKFNYDVNKRDKLDQQLMHVFSKLYPKITRDHNIDDNWKRGNYKMTRNQSEN 257
Qy	240 SKGVYCLQYDDEKIKISGLRDSNIKWDKTSLECLKVLTGTSVLCQYDERRVIVTSSD 299
Db	258 SKGVYCLQYDDEKIKISGLRDTNIKWDKDSCSRISLGHFTSVLCQYDNRVITSSD 317
Qy	300 STYRVWDVNTGEVNLTLIHHNPAVLHFLRFSNLMTCSKDRIAVMDASATDITLRLV
Db	318 RTVRWDVTEGCICKTLIHHCAVLHFLRANGIMVTCSKDRIAVMDVSPDITLRLV 377
Qy	360 VGHRAAVNWVDDDKYIVTVAASSGRTIKWSTCCEFRTLNGHKGRTACLQYQDRLVSG 419
Db	378 VGHRAAVNWVDDDRYIVSASSGRTIKWSTCCEFRTLNGHKGRTACLQYQDRLVSG 437
Qy	420 SSDNTIRLWDBCGACLRLVGEELYRCIRFDNKRTIVSGYDGKTKWWDQALDPRAP 479
Db	438 SSDNTIRLWDHSGVCLRLVGEELYRCIRFDKEKRTIVSGYDGKTKWWDQALDPRAL 497
Qy	480 ASTLCLRTLVEISGRVFLQDFEFQISSLSSDDTTLWDFEVPPSQNETRSPSRT 536
Db	498 SSEICLSSLVQHTGRVFLQDFQIVSSSSDDTTLWDFDAPPSS---LPSST 549
RESULT 3	
T50211	WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species:	Schizosaccharomyces pombe
C;Date:	09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 05-Oct-2004
C;Accession:	T50211
R;McBougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Jones, L.; Mc	
Qy	481 T38932 probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe)
Db	482 T38932 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Species:	Schizosaccharomyces pombe
C;Date:	03-Dec-1999
C;Accession:	T38932
R;Padcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.	
A;Reference number:	Z31818
A;Accession:	T38932
A;Status:	Preliminary; translated from GB/EMBL/DBJ
A;Molecule type:	DNA
A;Residues:	1-605 <BAD>
A;Cross-references:	UNIPROT:P87053; UNIPARC:UPI0000131DBA; EMBL:Z94864; PIDN:CA57A10
C;Genetics:	
A;Gene:	SPDB:SPAC57A10..05C
A;Map position:	1

Best Local Similarity 30.6%; Pred. No. 2.7e-36;	Matches 147; Conservative 85; Mismatches 167; Indels 82; Gaps 11;	Qy 62 KRPSEGN-----YOKEDL--CIIKYFDWSESSDQEVEHLLSRMCHYQGHHNNSYLK 112
Qy 108 NSYLKMLQLQRDFITALPEQGLDHIAENIISYLDARLCAELLVCKEWORVTSBEGMLWKKL 167	Db 117 KRTQEINANIAKLPQEISDIHHISKYSNSNDKAKLILDGILSTSCFPOLSYISSLVT 176	
Db 98 SSTLDLSIVRLDFSLIPLPE---ISFRILSFDARSUQAQVSXHWKELADDVWHRM 153	Qy 113 PMLQRFDTALPEQGLDHIAENIISYLDARSLCAELVCKEWORVTSBEGMLWKKLJERMV 172	
Qy 168 IER-----MVRTDPLWKGLSE-----RGGWDQY---LFKNRPTDG 199	Db 177 HMIKIDFISILPQE---LSLKILSTLDOSLCNATRVCKWQKLAADDDRWYHMCBQH 232	
Db 154 CEQHINKRKCEKGWGWLPLBERTLYAAKASQKRYERBLTQGVQHESSPVVKAKLDDY 213	Qy 173 RTDPWKGLSERR---GWDYLFKRN-----PTDGPNSFTRSLY 209	
Qy 200 P-----PNSFYRSLYP-----KLIQDIEETIESNWRCGRHNLQRIQCR- 236	Db 233 -----DRKCPNCGWGLPLJHMKRARIQNSTGSSSNADIQTQTTRMWKVYRERF 282	
Db 214 PTSSNEETISSLVSKPPSENDSKFPLFKTRPKWKEYAERCRVECHWRHGR-----CRQ 266	Qy 210 PKIQQDIEETLESNWRCGRHNLQRIQCRSENSK---GVYCLQYDDEKIIISGLRDNSIKW 265	
Qy 237 ---SENSKGIVYCLQYDDEKIIISGLRDNSIKWDKTSLECLKVLGTHTGSVLCLOYDERVI 293	Db 283 -----KVESNNWKG-----HCRIQFKGHMDGVLTQFNVRLLFTGSYSDTIGW 327	
Db 267 VVLSGHSIDGVNLQVNLNLLASGSYDFTIRLNLLATFOVALLEGHSVGTCLQFQCKL 326	Qy 266 DKTSLCECLKVLTGHTGSVLCLOYDERRVITGSSDSTVRWVDNTQEVLNLTJHHNEAVLH 325	
Qy 294 VTGSSPDSTRVYWDVNTGEVNTLHINHEAVLHLRFNSNGLMYTCSKDSRDIAYWDMASATDI 353	Db 328 DLFTGKLIRRUSLGHSDGVKTLFDDKLTKLSDLTDIRVNNYITGECISTYRGHSDSVLS 387	
Db 327 ISGSMDKTRIWNYRTSESCISLHLGHTDSVLCLTFTSLLVSGSADCTKVLWHFGGKR 386	Qy 326 LRFNSGLMYTCISKDSRDIAYWDMASATDLTERRVLLGHRAVNWVFFDKYI--VSAGSDR 403	
Qy 354 TLRRVLVGHRAAVNVYDF--DDKYIVSASGDRTIKWSSTSTCEFVRTLNGHKRGIACLQY 411	Db 388 VDSYKRVIVSADCTVWKWHVSESTCYTLR----GHTENWNCVLUHPKSFSCFSCSDTT 443	
Db 387 TLR---GHTGPVNNSVRIIRDRGLVLSGSDDSTIKWSLETNTCLHTESAHIGPVQSLAL 442	Qy 384 TIKWVSTSTCEFVRTLNGH--KRGIACLQYRD--RLVVSCSS-----421	
Qy 412 RDRLVVSGSSDNTIRLMDIECCACRVLGEHEELVRCIRDNKRYSGADGKIKWDLQ 471	Db 444 TIRMDIRNTSCLKVRGHVQVQKIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADE 503	
Db 443 ADSRLFSCSLDGTIKQWDIEKKCIVHFLFQHIGWEIAAHLRLISGAHDGVVXWEE- 500	Qy 422 -----DNTIRLMDIECGACLRLVJEGHEELVRCIRFDNK 454	
Qy 472 AALDPRAPASTLCLRTLVHEHSGRVRFLQDFEQITSSSHDFTLWDFLNPYPPSAONETR 531	Db 504 SDTPSNQETVLDENITPYTHLLSCLDNTIKLWDVKTGKCIIRTQFGHVGEWVDTAIDNF 563	
Db 501 -----ACECVHTLKHSEPVTSVALGDCEVSGSEDGKYLMLFNNAPNESPVSTQ 551	Qy 455 RIVSGAYDGGKIKWDLQAAQDPRAASTLCLRTLVHSGRVFRQLQDEFQFLQISSHDDTT 514	
Qy 532 S 532	Db 564 RIISGSHDGS1KWD1Q-----SGKGMHTF---NGR--RLORE-----TOHTQTO 603	
Db 552 S 552	Qy 515 LIWDFLNVPPA 526	
	Db 604 SLGD--KVAPIA 633	
RESULT 5	RESULT 6	
S49912 MET30 protein - yeast (Saccharomyces cerevisiae)	T46660 sulfur controller-2 protein [imported] - Neurospora crassa	
N; Alternate names: protein YIL9046w	C; Species: Neurospora crassa	
C; Saccharomyces cerevisiae	C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004	
C; Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 05-Oct-2004	C; Accession: T46660	
R; Odell, C.; Bowman, S.	R; Kumar, A.; Paietta, J.V.	
Submitted to the EMBL Data Library, December 1994	Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995	
A; Reference number: S49931	A; Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a	
A; Accession: S49932	A; Reference number: Z23121; PMID:3524199; PMID:7724564	
A; Molecule type: DNA	A; Map position: 3	
A; Residues: 1-640 <DB>	A; Map position: 3	
A; Cross-references: UNIPARC:UPI00012F726; GB:Z47047; EMBL:Z46861; NID:9	A; Introns: 75/3; 319/1; 354/1	
R; Thomas, D.; Cherest, H.; Barbet, R.; Surdin-Kerjan, Y.	C; Function:	
Submitted to the EMBL Data Library, December 1993	A; Description: negatively regulates sulfur structural gene expression	
A; Reference number: S49931	A; Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to the	
A; Accession: S49932	A; Gene: scn-2	
A; Molecule type: DNA	A; Gene: scon-2	
A; Residues: 1-60, 'I', 62-640 <DB>	A; Map position: 3	
A; Cross-references: UNIPARC:UPI0000168CD9; EMBL:L26505; NID:9432493; PID:9432494	A; Introns: 75/3; 319/1; 354/1	
C; Genetics:	Query Match 18.2%; Score 525; DB 2; Length 650;	
A; Gene: SGD:MET0	Best Local Similarity 24.2%; Pred. No. 8.7e-32;	
A; Cross-references: SGD:S0001308; MIPS:YIL046w	Mismatches 196; Indels 196; Gaps 16;	
A; Map position: 9L	Matches 155; Conservative 93; Mismatches 196; Indels 196; Gaps 16;	
P; 298-329/Domain: WD repeat homology <WD1>	Qy 38 CLQMSVRCVQIQSINGTSSVSRCPSEGNYQKERDLC1KYFDWSESDQVEFFEH---94	
P; 338-369/Domain: WD repeat homology <WD2>	44 CYRHHDSDKCRRAADKAKMNM-----QSE-----LDLUTSADQ-QAVTHWVS 85	
F; 374-409/Domain: WD repeat homology <WD3>		
F; 417-450/Domain: WD repeat homology <WD4>		
Query Match 18.4%; Score 528; DB 2; Length 640;		
Best Local Similarity 28.4%; Pred. No. 8.9e-33; Mismatches 166; Indels 142; Gaps 19;		
Matches 157; Conservative 87; Mismatches 166; Indels 142; Gaps 19;		

Qy	95 -----LISRMCHYQHGHINSYLKPEQLORDFITALPEQOLDHIAENTILSY 138	Db	120 TGLIVTASSDRTRLRTWDITTCIRGCIRIWTAAHORCIACAGYNGKEPVSGSSDLTRIFEAASS 179
Db	86 LFSAPAPRHDMLQGILSOLCFPQLSFSTREVNBEALKDFISALPVE --- -IAQRVLCY 141	Qy	433 GACLRVLGEHEELVRCTRFDNKRIVSGAYDGKIKWDLQAALDPRAPASTLICRLTVERH- 491
Qy	139 LDARSLLCAELVCKEWORYVISEGMLWKKLIERMYR- -TDPLN- KGLSERRGHDQYLEPKFN 194	Db	180 GKLLRMLQGHEDLIRTVRENDEKIVSSGCGYDGTIVRN----- -FNTGEQHK 224
Db	142 LDVTSLLTKAAQVSQRWRTIADSDAWVRCHEQHYNRKCTKCGNGLPLIERRKLNRNYTRQR 201	Qy	492 -----SGRFLQFDEFQFISSHHDDTLIWD 519
Qy	195 RPTOPP----- -NSFYRSL- --- YP 210	Db	225 VLHNSRNSRVFGQLQFDHRIIACTHSSEILWWNF 258
Db	202 QLAKGPGQRVTELADSHBDSODRSVNHQGRPAAEAEEDPIKRCQMAAAEASKAVTQP 261		
Qy	211 K-----IQQDIEETESNWRCGRHNLORIQCERSENSKGYVGYCLOYDDEKEISIGLDRNSIKI 264		RESULT 8
Db	262 KTRSKRAVVRDRMWSVSYNWNNSRYSKLSVK--- -SHENGTYCLODDNLTATGSDTFTKI 318		T22703 hypothetical protein F55B12.3 - Caenorhabditis elegans
Qy	265 WDXTSLECKVLTKHTGSVCLQYDDEVITVGSSDSTVYVWDTNTGEVILNLTHHNEAVL 324		C;Species: Caenorhabditis elegans
Db	3119 WNIETEECARTLVGTAGTRALQFDSSKLGSDHTKWWNHTGECLSTFAAHTDSVI 378		C;Date: 15-Oct-1999 #text_change 09-Jul-2004
Qy	325 HLRPSNGLWAVTCSDRSIAWMDMASATDTLRRVLUHGHAANVY- -VDDDDKTVIASGD 382		C;Accession: T22703 #sequence_revision 15-Oct-1999
Db	3797 SVHEDGHLASGSSDKTVKIDFNSKETVCLK-- -GHSDWNSRTHDIKSRTVFEASD 434		R;Sims, M.
Qy	383 RTIKWVSTSTCEFYRTLNGHKGRTI----- -ACLYQRDRLVYV----- 418		Submitted to the EMBL Data Library, September 1996
Db	435 TTKLWDLTRQVIRTYEGVGHVQVQLLPPPEYEPDEEVNGASQNDAMSVSSGSSG 494		A;Reference number: Z19602
Qy	419 ----- G 419		A;Accession: T22703
Db	495 SPSMSHAQ1ERAGSPGSHSSHNNLJPSSLPSGQDDEVRLPPTYFNG 554		A;Status: preliminary; translated from GB/EMBL/DBBJ
Qy	420 SSDNTIRLWIECGACLRVLEGHEELVRCTRFDNKRIVSGAYDGKIKWDLQAALDPRAP 479		A;Cross-references: UNIPROT:Q93794; UNIPARC:UPI000135742; EMBL:Z79757; PIDN:CA02129.1;
Db	555 GLDSTMRLNDSATGRCLRTLFGHLEGWMSLAGDTTRVISGANDGMVKTWE----- P 605		A;Genetics:
Qy	480 ASTLCLTURLYEHSGRVRFLQFDEFQFISSHHDDTLIWD 519		A;Gene: CESP.F55B12.3
Db	606 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		A;Map position: 5
Qy	607 -----		A;Map position: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1
Db	608 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		A;Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1
Qy	609 -----		Query Match 17.8%; Score 512; DB 2; Length 579;
Db	610 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		Best Local Similarity 27.5%; Pred. No. 7.2e-31; Matches 146; Conservative 77; Mismatches 206; Gaps 15;
Qy	611 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		Qy 51 SNGTSSVIVSRKPSBEGNYQKEDL----- -C1KFDQWSESDQVEFVBH 94
Db	612 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		31 SNGGSSSYNAKDUSSSRPQHQUDSASPSRNNDLNPRVHEVHTALFKDLSSEAOMDAFR 90
Qy	613 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		Qy 95 LISRMCHYQHGHNSYKLEMQLRDFFITALPEQDHIAENILSYDARSLLCAELVCKEW 154
Db	614 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		91 LLQBSNMNINIQRLRAIIIEPHFQDFLSCLPVE-- -LGMKILRNLTGYDLKVAQVSXNW 146
Qy	615 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		Qy 155 QRYTSEGMIWKKLJEBMRDPLWKGLSERRGWDQYLFKNRPTDPNSF----- 204
Db	616 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		147 -KLISE----- -IDKWLKSL----GVEEFKHPDPIDTRVGAQWQTAAGVT 188
Qy	617 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		205 ----- -YRSLYPKIIQD----- -ETIESWRCGRHNQLRIO----- C 235
Db	618 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		189 IPDHQPCDINVIRFKLQKFQGDFLERAADKSRYLRADIEKW----- -NANPMGSAVL 243
Qy	619 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		236 RSENKGYCYCLOYDDEKITSLECLKVTGHTGSVCLQYD----- RVI 293
Db	620 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		244 RGHDHVITCMQIHDDVLTGSDNTLKVWCIDKGEMVYTLVGHGTGGWTSQSQGRYI 303
Qy	621 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		294 VTSGSDSTSIVRWVHDNTGEVLTJLJHNEAYLHLRFNSGLMVTCSDRSIAWMDMASATDI 353
Db	622 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		304 VSGTDRITKWSVTPVGSLSLHTQGHTSSTVRCNAMAGSILVTSRDTLIRWVDESGRHL 363
Qy	623 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		354 TLRRVUGHRRAAVNVVDPPDKYIVASGDRTIKWTSTCFCYRTLNGHKGRIAOLQYRD 413
Db	624 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		364 A---TLRGHHAAVRCVOPFGTIVVGGDFTVCIWNAFTGCRCLRTLGHINRYSLLFES 420
Qy	625 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		414 R-LIVVSGSSDNTRLWDI---EGGACARVLEGEHELYRCIRGFDNKRTVSGAYDGKIKW 468
Db	626 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		421 ERSIVCGSLDTSIRWMDTRPREGOCVALLQGHTSLSGMQLRGNLVSCNAHSVVRW 480
Qy	627 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		469 DLOQALDPRAPASTLCLRTLVEHESGRVRFLQ-FDFOLISSSHDDTILW 51.8
Db	628 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		481 DIHEG----- -TCVHMLSGHSRSAITSLQWGRNMVATSSDDGTVKLWD 522
Qy	629 RSGKDATTGHCGVFTCVGLSDLSMASSEDGTIRLHST 645		375 --YIVSAGDRTIKWSTSTCEFVRLNGHKGRIAOLQYDRLVVGSSSDNTIRLWDIBC 432

RESULT 9

T18521 beta transducin-like protein - *Podospora anserina*C;Species: *Podospora anserina*

C;Accession: T18521 Date: 15-Oct-1999 #text_change 09-Jul-2004

R;Saupe, S.; Turcq, B.; Begueret, J.

Gene: 1-135 1995

A;Title: A gene responsible for vegetative incompatibility in the fungus *Podospora anserina*

A;Reference number: Z18944; MUID:96009891; PMID:7557402

A;Status: preliminary; translated from GB/EMBL/DDBj

A;Molecule type: DNA

A;Residues: 1-135 <SAU>

A;Cross-references: UNIPARC:UPI000808; UNIPARC:UPI00012C621; EMBL:L28125; NID:9607002; PID:

C;Genetics:

A;Gene: her-e1

A;Introns: 761/3

A;Protein popl: 16.3%; Score 468.5; DB 2; Length 1356;

A;Best Local Similarity 28.7%; Pred. No. 4.6e-7; Mismatches 189; Indels 95; Gaps 20; Matches 144; Conservative 74; Gaps 20;

A;Query Match 76 CIKYFDQWSESPQVEFVHLISRMRCH--YOHGHIN---SYLKPKMLQRFDTALPEOGL 128

A;Db 698 CIYWDHLR----DLVSTSSKWHVLQDDCDIHRFLTTKYLWDEALSLLRAPE-GI 751

A;Qy 129 DHI-AENITLSYLDARSLSCAAELVKCKEWQRVISSEGMIWKKLIERMYRTDPLWKGLSERG 186

A;Db 752 NAIRQLESLIIGLHTGRHLA-----IVRDGYRFALSYRMILIEKAP!QAYTS--- 797

A;Qy 187 WDQYLFKRNPRIDGPNSFYRSRSLYPKLIQDIETIESNWRGRHNL---- 230

A;Db 798 -ALVF-APIDSMIKKIFKEPKGMWISTISVVEATNACTQTLLEGHGSVLSVAFAADG 853

A;Qy 231 QRIQCRSENSK-----GVCYCLQY-DDEEKITISGLDRDNSTIKWIKDT 268

A;Db 854 QRVASGSDDKTIIKIWDTAAGTGTQTLLEGHGSVWSVAFSPDRERAVASGDDDTKIKWDA 913

A;Qy 269 SLECLKVLTGHTGGSVSLCQY-DERIVTGSSDSTVRWMDNTGEVNTLHHNEAVHL 326

A;Db 914 SGCTCTQTLLEGHGSVGRVQSGORVASSPDSGQVASSPDRERAVASGDDDTKIKWDA 973

A;Qy 327 RFS-NGLMVTC-SKDRSIAWWDMA5ATDITURRVLGHRRAAVNVVDPE-DDKVIYASGD 382

A;Db 974 AFSPDGORVASSGSDKTTIKINDTASG---TCTQTLLEGHGSVWSVAFSPDGQVASSGDD 1030

A;Qy 383 RTIKWNSTSTCFVRTLNHGKRGIACTQYR-DRLVGSSDNTIRLWDTIECGACIYRLV 440

A;Db 1031 KTKIKWDTAAGTGTQTLLEGHGSVWQSIVFSPDGQVASSGDDDTKIKWDAVGTCQTQLE 1090

A;Qy 441 GHEELVRCIRF-DNKRIVSGAYDGKIKWMDLQQAALPRAPASTCLRLTVEHSERVERL 498

A;Db 1091 GHGDSWVAFSPDGQVASSGDDDTKIKWDAVGTCQTQLEGHGGMVHSV 1141

A;Qy 499 QF--DEFOQISSHDDTILWD 518

A;Db 1142 AFSPDGORVASSGSDKTTIKWDA 1163

RESULT 11

AE1810

WD-40 repeat protein [imported] - *Nostoc* sp. (strain PCC 7120)C;Species: *Nostoc* sp. PCC 7120A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001

C;Accession: AE1810

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Status: preliminary

A;Molecule type: DNA

RESULT 10

T45136 WD repeat protein popl [imported] - fission yeast (*Schizosaccharomyces pombe*)C;Species: *Schizosaccharomyces pombe*

C;Accession: T45136 Date: 21-Jan-2000 #text_change 21-Jan-2000

R;Kominnami, K.; Toda, T.

A;Description: Fission yeast WD repeat protein Pop1 is involved in maintenance of ploidy

A;Reference number: Z22925

A;Status: preliminary; translated from GB/EMBL/DDBj

A;Molecule type: DNA

A;Residues: 1-1227 <KUR>
A;Cross-references: UNIPROT:Q8Z0R1; UNIPARC:UPI00000CDBE5; GB:BA000019; PIDN:BAB7753.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0029

Query Match 14.8%; Score 425; DB 2; Length 1227;
Best Local Similarity 25.3%; Pred. No. 7.9e-24;
Matches 139; Conservative 106; Mismatches 192; Indels 112; Gaps 23;

Qy 23 WLGANLVESSMCALSCLOSMPSVRCLQISNGTSSVIVSRKRPSGNYQKE----KDLC 76
Db 401 WLTTESPKVKMEALSLRR-----SLEKASPLIEKASSTGEAEKKFGLSENV 454

Qy 77 KYFDQWSSESDQVEFHILTSRMCHYQHGHINSYKPMWQDFITALPQGLDRIAENL 136
Db 455 MEYI-----TAKPIENSLEEF-----SQTKKL---DFNTYP----- 483

Qy 137 SYLDARSLCAAEYLCKEWORVISEGMLWKKL-----IERMVRTDPLWKCOLSERG 186
Db 484 -LMKARSL---DYIRQIQLILEVKQULNIFGTTELBIHLRMIGT-LQEPLPKKG 537

Qy 187 W-----DQYLFKNRNPNDGPNSFYRL-----YPTKIQDENTIESNWRCGRHN 229
Db 538 YAAGNLLNLRLQOLDKIPDESPIDLSGDFSGLTIQKFYKLTKEITIFAN-----SD 592

Qy 230 LQRQCRRSENKGVCLQI-----DDEKLISGARDNSIKIWKTSLECLVLTGHTGSVLCQ 287
Db 593 LTG-SVFTETMSSVSVKSPDGKYFATGMNGEIRLWTSNDKQLYKHTAWWWAFA 651

Qy 288 Y--DERRVYTGGSDSTVRYWDVNTCEVLNLTHHEAVLHLRFS--NGIMVMTCSKDRSA 343
Db 652 FSPDSRMLASGADSTIKMDVHTECLTKLTSRNTNRTVSAFSPDGRLIASQDQTK 711

Qy 344 VWDMASATDITLRRVLYGHRAAVNVDF---DDK--YIVSASSDRTIKWWSSTCTCFVR 397
Db 712 LWDTATG---NCQOPLIGHDWWNSVTSVTDDPLLASSADQHKLWDAVGKCK 768

Qy 398 TLNGKRGKACLQYR--DRLVSGSSDNTRLWDECGACLRVLEGEHEELVRICRE--DN 453
Db 769 TLKGHTREVHSVSFSPDGQTLASSGBSDSTVRLWDVKTGCGCWOLFEGHSCKVSYRFSPG 828

Qy 454 KRVSGAYGDKIKWDLQQAIDPRAPISTLCLRTLVHEHSSRVERLQF--DEFQLISSHD 511
Db 829 QTLASCGEDRSIKMDIQRG-----ECVNTLWGHSSQVMIAFSPDGRTJUSCSDD 879

Qy 512 DTLLIWDFL 520
Db 880 QTARLWDFI 888

RESULT 12

S56145 cell division control protein CDC4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YFL009w
C;Species: Saccharomyces cerevisiae
C;Accession: S56245; S48310; A26867; S62304
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasano
R;Submitted to the EMBL Data Library, September 1994
A;Reference number: S56186
A;Accession: S56245
A;Residues: 1-779 <MUR>
A;Cross-references: UNIPROT:PO7834; UNIPARC:UPI0000127254; EMBL:D50617; NID:9836685; PIDN:CAA29113.1; PID:3309335

RESULT 13

T43557 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: proteolysis factor sup1P
C;Species: Schizosaccharomyces pombe
C;Accession: S48310
A;Molecule type: DNA
A;Residues: 1-579 <CHU>
A;Cross-references: UNIPARC:UPI0000168AE; EMBL:Z46255; NID:9559925; PIDN:CAA86341.1; PID:21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43557; T38794; T43798

R; Wolf, D.A.; Jackson, P.K.	Submitted to the EMBL Data Library, December 1997
A; Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in th	
A; Reference number: 222576	
A; Accession: T4557	
A; Status: preliminary; translated from GB/EMBL/DDJB	
A; Molecule type: mRNA	
A; Residues: 1-703 <WOL>	
A; Cross-references: UNIPARC:O14170; UNIPARC:UPI0000131F36; EMBL:AF038867; PIDN:AAE95480.	
A; Experimental source: strain h- 972; R; Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.	
A; Reference number: 221812	
A; Accession: T38794	
A; Status: preliminary; translated from GB/EMBL/DDJB	
A; Molecule type: DNA	
A; Residues: 1-703 <GEN>	
A; Cross-references: UNIPARC:UPI0000131F36; EMBL:298602; PIDN:CA011275.1; GSPDB:GN00066;	
A; Experimental source: strain 972h ; cosmid c4D7	
R; Jallepalli, P.V.; Tien, D.; Kelly, T.J.	
Proc. Natl. Acad. Sci. U.S.A., 95, 8159-8164, 1998	
A; Title: Stud1+ targets cyclin-dependent kinase phosphorylated Cdc18 and Rum1 proteins fo	
A; Reference number: 222686; PMID:98318628;	
A; Accession: T41298	
A; Status: preliminary;	
A; Molecule type: DNA	
A; Residues: 1-703 <JAL>	
A; Cross-references: UNIPARC:UPI0000131F36; EMBL:AF064515; NID:93293382; PIDN: AAC39496.1;	
C; Genetics:	
A; Gene: pop2; std1; SPAC4D7.03	
A; Map position: 1	
C; Function:	
A; Description: required to prevent spontaneous re-replication	
Query Match Score 389.5; DB 2; Length 703;	
Best Local Similarity 23.3%; Prd. No. 1; Re-21;	
Matches 143; Conservative 113; Mismatches 231; Indels 127; Gaps 25;	
Db 114 pDSVIEDKTIELMCSPVRSLWLGCAANLYVSMCAL-SCLQSMPSVRCLQISNGTSS---- 56	
Db 114 pDSVGDNSFISL---VPQ----RNFLYSHSSLPLPKTISIDRNRRKTLDNSSNSDNF 164	
Qy 57 ---VIVSRKRPSGEVNYQREKDL-----CIIYKFQDWSESDDOVEFVHLLISRMCHYQH 105	
Db 165 PPSPKVDTNTVSPGSKPISEDLDLNQSIYQTPEDLPREGIQ-SYAFFQLRSCNRQSM 223	
Qy 106 H-INSVKLPMQLDFITALPEQGLDHIAENILSYLDARSCLCAABLVCKEWQRVTS-EGML 163	
Db 224 RLLNECPLRKDIILSPFS---IIVSILNLDIHSFLSCLPSPTRNRLDVHTSY 279	
Qy 164 WKKLIE---RMRVTRDPLWKGLSERRGMQYLFKNRPTDGP-PNSFYRS-----LYPK 211	
Db 280 WKKMFSLFGQINEND--WKYANPNLNARPPFLNDOLSDDYFEEFKHFLNRKRWLFFPS 337	
Qy 212 IIQD-----IBTIESWRGRGHNLQR--ICRSENKR-GYCL 246	
Db 338 IPPSHLSPPIHYPNFMITSLLHKDRITTSGGTQIHNAITGVLEARLEGKEGWAV 397	
Qy 247 QYDEDEKLISGLDANSIKIWWDKTSLECLKVLGHTGTVSLQY-----DE 290	
Db 398 KIHTNLVSGISDKTVRWNIEKACTHFRGHSITIRCLTELVPSLRIRHGGEIVEEDQ 457	
Qy 291 RVITVGSSDSTVWWDV-----INTLIIHNEAVHLRFPSN 330	
Db 458 PYIVSGSRDHTLRRWKLPKNTDPYLPDNTNSLDRWEKPYFVHTLIGHTDSVRTISGYG 517	
Qy 331 GLMVTCRKDRSIAWDMASATDITLRRVYLGHRRAVNVDFFDDK--VIVSASCDRTIKW 388	
Db 518 DIVSGSYDSSTRIWRVSTGECIYHLR--GHSU1RIVSYLVEPNRNICISGSMDKSIRW 574	
Qy 389 - STSTCEFPVRLNGHKGJACQYRDRBLVUVSSSDNTLRLDIEGAQLRVLEGEHELV 446	
Db 575 DLSGTGTCXY--LEGHDAYFTVUNFONRLISSADSTTRIWLNGKPLMYSNNSXLY 632	
RESULT 15	
AC1842	
WD-40 repeat protein [Imported] - Nostoc sp. (strain PCC 7120)	
C; Species: Nostoc sp. PCC 7120	
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120	
C; Accession: AC1842	
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Takazawa, M.; Yasuda, M.; Tabata, S.	
DNA Res. 8, 205-213, 2001	
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An	
A; Reference number: AB1807; MUID:21595585; PMID:11759840	

A;Accession: AC1842
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1747 <KUR>
 A;Cross-references: UNIPROT:Q8Z020; UNIPARC:UPI00000CDCC1; GB:BA0000019; PIDN:BAB77807.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: All0283

Query Match Score 383.5; DB 2; Length 1747;
 Best Local Similarity 33.5%; Pred. No. 1.8e-20;
 Matches 8; Conservative 51; Mismatches 99; Indels 19; Gaps 8;

Qy	229	NLQRQCRSENSKGWYCLQY-	-DDEKIISSLRDNNSIKIWDKTSLECLKWLTTGHTGSVLT	L 286
Db	1468	SLSTIQ--KNQNLITTVSPDGKTIATASADNTIKIWDSDQTOQLIKLTGHKDRTTL	1524	
Qy	287	QY--DERRVVTGSSDSTVRVWDVNTEVINTLIIHNEAWLHLRS--NGLMVTCSKDRSI	342	
Db	1525	SFHPDNOTLASGADKTICKWRYNDGQLLRTLGHNDETSVNEFSPDGFLASGGSTDNTV	1584	
Qy	343	AVWDMASATDITLRRVLYCHRAAVNVDF--DDKIVSASGDRITKWSSTSTCBFVRTLN	400	
Db	1585	KIWO---TDGRLKNIITGGLAASVKSPDSHTLASWDNTIKLWVTDGKLINNNLN	1640	
Qy	401	GHKGIGIACIQR--DRLVVSQGSSDNTIRLWIEGACFLVLEGHBELVCIRF--DNKRI	456	
Db	1641	GHIDGVTSISFSFDGBILASGSADNTIKLWNLPNATLKLGHPGKINTLAFLSPDGKTL	1700	
Qy	457	VSGAVDGGKIRWDL 470		
Db	1701	LSGGBDAGVNWNL 1714		

Search completed: August 25, 2006, 07:23:15
 Job time : 44 secs

Scoring table:	BLOSUM62						
Searched:	Gapext 0.5						
Total number of hits satisfying chosen parameters:	2849598						
Minimum DB seq length:	0						
Maximum DB seq length:	200000000						
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries						
Database :	UniProt 7.2: 1: uniprot_spdbot;* 2: uniprot_trembl;*						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
1	2879	100.0	542	1	FBW1B_HUMAN	Q9ub1	homo sapien
2	2851.5	99.8	542	2	QSSRY7_MOUSE	Q8k022	mus musculu
3	2851.5	99.0	563	2	Q923H0_MOUSE	Q923H0	mus musculu
4	2755.5	95.7	563	2	Q3TLZ8_MOUSE	Q8By90	mus musculu
5	2664.5	92.6	529	2	Q3TGM9_MOUSE	Q3tgm9	mus musculu
6	2664.5	92.5	529	2	Q3TGM9_MOUSE	Q3tgm9	mus musculu
7	2660	92.4	508	2	Q3TGM9_MOUSE	Q8chD5	mus musculu
8	2652.5	92.1	529	2	Q5ZH02_CHICK	Q5zgq9	gallus gallus
10	2448.5	85.0	527	2	Q6PGW4_BRARE	Q6pgw4	brachydanio
11	2445.5	84.9	605	1	FBW1A_HUMAN	Q9y297	homo sapien
12	2445.5	84.9	605	1	Q5W141_HUMAN	Q5w141	homo sapien
13	2437.5	84.7	605	2	Q3UL2_2_MOUSE	Q3ul12	mus musculu
14	2436.5	84.6	639	2	Q571K6_MOUSE	Q571K6	mus musculu
15	2434.4	84.5	564	2	Q6DSO0_HUMAN	Q6ds00	homo sapien
16	2429.5	84.4	605	2	Q5RDW6_PONY	Q5rdw6	pongo pygma
17	2423	84.2	527	2	Q7VZL1_BRACHY	Q7vzl1	brachydanio
18	24.03	83.5	587	2	Q4R626_MACPFA	Q4r626	macaca fasc
19	2384.5	82.8	569	2	Q5W142_HUMAN	Q5w142	homo sapien
20	2375.5	82.5	569	2	Q9QK15_MOUSE	Q9qk15	mus musculu
21	2368.5	82.3	569	2	Q9QK15_MOUSE	Q9qk15	mus musculu
22	23.62	82.0	553	2	Q3U004_MOUSE	Q3u004	mus musculu
23	23.55	81.9	569	2	Q9R1G7_MOUSE	Q9r1g7	mus musculu
24	23.53	81.7	506	2	Q5UE5_RAT	Q5ue5	rattus norv
25	23.01	79.9	518	1	TRCB_XENLA	Q91854	xenopus lae
26	23.01	79.9	518	2	Q6AX69_XENLA	Q6ax69	xenopus lae
27	21.57	74.9	440	2	Q4TB8J7_TETNG	Q4tb8j7	tetraodon n
28	21.14.5	73.4	621	2	Q8ESD3_CIGOTN	Q8esd3	ciona intes
29	20.77.5	72.2	510	2	Q443B2_DROME	Q443b2	drosophila
30	20.77.5	72.2	510	2	Q9VDE3_DROME	Q9vde3	drosophila
31	2039.5	70.8	514	2	Q7PYH7_ANOGGA	Q7pyh7	anopheles g

		MEDONEDESPKONTW (in isoform B).
PT	FT	FTID=VSP 00676.
RA	FT	FTID=VSP 00676.
RA	SEQUENCE	542 AA; 62091 MW; 7CD40087EFAA5C8A CRC64;
RA	Query Match	100.0% ; Score 2879 ; DB 1 ; Length 542 ;
RA	Best Local Similarity	100.0% ; Pred. No. 8.3e-205 ;
RA	Matches	0 ; Mis matches 0 ; Indels 0 ; Gaps 0 ;
RA	Conservative	542 ;
RA	MEPDSTIEDKTIELMCSVPRSLWLGCANLVESMCALSQLSMPSVRCLQTSNGTSIVS 60	
RA	MEPDSTIEDKTIELMCSVPRSLWLGCANLVESMCALSQLSMPSVRCLQTSNGTSIVS 60	
RA	Db	1 MEKPSEGYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Db	61 RKRPSGEYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Db	61 RKRPSGEYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Qy	1 MEPDSTIEDKTIELMCSVPRSLWLGCANLVESMCALSQLSMPSVRCLQTSNGTSIVS 60
RA	Db	1 MEKPSEGYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Qy	61 RKRPSGEYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Db	61 RKRPSGEYQKEKDLCIKYFQDWSSEDOVEFVHLISMCHYQHNSYLKPMQLRDFI 120
RA	Qy	121 TALPEQGLDHIAENILSYLDARSCLAAELVKCKEWQRVISEGMLWKLKLIBRMVRTPLWKG 180
RA	Db	121 TALPEQGLDHIAENILSYLDARSCLAAELVKCKEWQRVISEGMLWKLKLIBRMVRTPLWKG 180
RA	Qy	121 TALPEQGLDHIAENILSYLDARSCLAAELVKCKEWQRVISEGMLWKLKLIBRMVRTPLWKG 180
CC	CC	-!- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation. May participate in Wnt signaling.
CC	CC	-!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex.
CC	CC	-!- SUBCELLULAR LOCATION: Cytoplasm (Potential).
CC	CC	-!- ALTERNATIVE PRODUCTS:
CC	CC	Event=Alternative splicing; Named isoforms=3;
CC	CC	Name=C;
CC	CC	IsoId=9Ukb1_1; Sequence=Displayed;
CC	CC	Name=A;
CC	CC	IsoId=9Ukb1_2; Sequence=VSP_006765;
CC	CC	Name=B;
CC	CC	IsoId=9Ukb1_3; Sequence=VSP_006766;
CC	CC	-!- SIMILARITY: Contains 1 F-box domain.
CC	CC	-!- SIMILARITY: Contains 7 WD repeats.
CC	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	CC	-----
CC	CC	EMBL; AF176022; AA04528.1; - ; mRNA.
CC	CC	DR ENSEMBL; AB033229; BA092329.1; - ; mRNA.
CC	CC	DR ENSEMBL; BA092330.1; - ; mRNA.
CC	CC	DR ENSEMBL; AB033281; BA092331.1; - ; mRNA.
CC	CC	DR ENSEMBL; AB014596; BA031167.1; ALT INIT; mRNA.
CC	CC	DR ENSEMBL; BC026213; AA026213.1; - ; mRNA.
CC	CC	DR HSSP; QBY297.1P22.
CC	CC	DR Ensembl; ENSG00000072803; Homo sapiens.
CC	CC	DR InNDDB; HIX0005413.1; - .
CC	CC	DR HGNC; HGNC:13607; FBXW11.
CC	CC	DR MIM; 605511; Gene.
CC	CC	DR LinkHub; Q9URK1; - .
CC	CC	DR GO; GO:0000151; Cubiquitin ligase complex; NAS.
CC	CC	DR GO; GO:005515; Protein binding; IPI.
CC	CC	DR GO; GO:004812; F:Protein ligase activity; NAS.
CC	CC	DR GO; GO:0016567; Ubiquitin-protein ligase activity; NAS.
CC	CC	DR InterPro; IPR001810; F-box.
CC	CC	DR InterPro; IPR001680; WD-0.
CC	CC	DR PFAM; PF00646; F-box; 1.
CC	CC	DR PFAM; PF0400; WD4; 7.
CC	CC	DR PRINTS; PR00320; GROTEINBRPT.
CC	CC	DR PRODOM; PD000018; WD40; 4.
CC	CC	DR SMART; SM00256; FBXK; 1.
CC	CC	DR SMART; SM00320; WD40; 7.
CC	CC	DR PROSITE; PS50181; PBOX; 1.
CC	CC	DR PROSITE; PS00678; WD_REPEATS; 1; 5.
CC	CC	DR PROSITE; PS50082; WD_REPEATS; 2; 7.
CC	CC	DR PROSITE; PS50294; WD_REPEATS; REGION; 1.
KW	KW	Alternative splicing; Repeat; Ubl conjugation pathway; WD repeat; Wnt signaling pathway.
FT	CHAIN	1 542 F-box/WD-repeat protein 11.
FT	DOMAIN	129 167 F-box.
FT	REPEAT	238 275 WD 1.
FT	REPEAT	278 315 WD 2.
FT	REPEAT	318 355 WD 3.
FT	REPEAT	361 398 WD 4.
FT	REPEAT	401 440 WD 5.
FT	REPEAT	442 478 WD 6.
FT	REPEAT	490 527 WD 7.
FT	VARSPLIC	16 49 Missing (in isoform A).
FT	VARSPLIC	16 48 Missing (in isoform A).
FT	VARSPLIC	16 48 CSVPRLWVAGANLYVESMCALSQLSMPSVRCL->NTVS.

- [3] RN NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
MEDLINE=9927953; PubMed=10349336; DOI=10.1016/S0076-6879(99)03004-9;
- RA Maglott D.R., Maltais K., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata T., Okido T., Pavan W.J., Partea G., Pesole G.,
RC Petrovsky N., Pillai R., Pontius J.U., Qi D., Ranachandran S.,
RX Ravaci T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C.A., Semple C.A., Setou M., Shimada K.,
RA Sultan A., Takehara Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RL Methods Enzymol. 303:19-44 (1999). ;
- RN NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
RX Ambesi-Implombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beise K.W., Bersano T., Bono H., Chaik A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingers T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelenck L., Iacono M., Ikeyo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollins G., Krishnan S.P., Kruger D., Kummerfeld S.K.,
RA Kuroochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Migone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,
RA Nilsson P., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando J., Pang K.C., Pavic W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiyra K., Sulcana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashita H., Zabro茨ky B., Zhu S., Zimmer A., Hidé W., Bult C.,
RA Grimaldi S.M., Teasdale R.D., Liu B.T., Kauri C., Sasaki D.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagishiura N.,
RA Kawashima T., Koijima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watanuki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
Science 309:1559-1563 (2005). ;
- RN NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
RX PubMed=16141073; DOI=10.1126/science.1112009;
- RG RIKEN Genome Exploration Research Group, and Genome Science Group
(Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RN Science 309:1564-1566 (2005). ;
- RN NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion;
RX MEDLINE=22354683; PubMed=146651; DOI=10.1038/nature01266;
- RG Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osako N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami T., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frater K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Hough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA	Muramatsu M., Hayashizaki Y. ;	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC	Copyright by the UniProt Consortium, see http://www.uniprot.org/terms	Distributed under the Creative Commons Attribution-NoDerivs License
CC		
DR	EMBL; AL669951; CBA126097.1; -; Genomic DNA.	
DR	EMBL; AL669844; CBA12550.1; -; Genomic DNA.	
DR	EMBL; AL669951; CBA12550.1; -; Genomic DNA.	
DR	EMBL; AR149139; BAE28749.1; -; mRNA.	
DR	Ensembl; ENSMUSG00000020271; Mus musculus.	
DR	GO:0006512; P:ubiquitin cycle; IEA.	
DR	InterPro; IPR01810; F-box.	
DR	Pfam; PF00646; F-box; 1.	
DR	PFam; PF04040; WD40; 7.	
DR	PRINTS; PR00320; QPROTINBRRRT.	
DR	ProDom; PD000018; WD40; 4.	
SMART	SM00256; FBOX; 1.	
SMART	SM00320; WD40; 7.	
DR	PROSITE; PS50181; FBOX; 1.	
DR	PROSITE; PS00678; WD_REPEATS_1; 5.	
DR	PROSITE; PS00682; WD_REPEATS_2; 7.	
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KW	Repeat; Upf conjugation pathway; WD repeat.	
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Db	1 MEPSVIEDEKTIELMCSVRSLWGANLIVESMALSQSMSSVRCLQISNGTSSVIVS 60	Best Local Similarity 99.6%; Pre. No. 2.8e-20; Indels 0; Gaps 0; Matches 540; Conservative 2; Mismatches 0;
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Qy	121 TALPFGGLDHAENILSYLDARSLSCAAELVKKEYQRVISSEGMLMKKLTERMVTDPLMKG 180	
Db	121 TALPQGLDHAENILSYLDARSLSCAAELVKKEYQRVISSEGMLMKKLTERMVTDPLKG 180	
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Db	421 SDNTIRLMDIECGACIYRLVCFRTINGHKGIAQYRQLRVWSG 480	
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Db	481 STLCLRTLVHSGRVERLQDEFQIISSHDDTLLWDFLNVPSSAQNETRSRSPRTYYI 540	
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Db	541 SR 542	Best Local Similarity 95.9%; Pred. No. 9.e-203; Mismatches 0; Index 21; Gaps 1;

- OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX RN [1]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 Carninci P., Hayashizaki Y.,
 Methods Enzymol. 303:19-44 (1999).
 RN [2]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 PubMed=16141072; DOI=10.1126/science.1112014;
 Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodis R., Shimokawa K.,
 Bajic V.B., Brenner S.B., Batyalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilming L.G., Aedinis V., Allen J.B.,
 Ambesi-Impemba A., Apweiler R., Auraliya R.N., Bailey T.L.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Crowe M.L., Dalla E., Dalrymple B.P., Clutterbuck D.R.,
 di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Garibaldi M.,
 Georgii-Hemming P., Gingera T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill M., Huminiecki L., Iacono M., Ieko K., Iwama A., Ishikawa T.,
 Jait M., Kanapin A., Katch M., Kawasawa S., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kuroianchi I.V., Lareau L.F., Lazarevic D., Lipowich L., Liu J.,
 Liuni S., McWilliam S., Madden Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Miyagone F., Miyake S., Morris K.,
 Motaguchi-Tabar S., Mulder N., Nakano N., Nakauchi K., Ng P.,
 Nilsson R., Nishimichi S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Parva W.J., Pavese G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibusawa Y., Shimada K., Shigada K., Silitana R., Takemoto Y., Taki K.,
 Sperling S., Stupka E., Sugiyra K., Suzuki D., Sinclair B.,
 Tammoja K., Tar S.L., Tang S., Taylor M.S., Tegnér J., Techmann S.A.,
 Ueda H., van Nieuwegen E., Verardo R., Wei C.L., Yegi K.,
 Yamamoto H., Zabavovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Grimmond S.M., Tessdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Matlick J.S., Hume D., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Koijima M., Kondo S., Konno H., Nakano K., Nomiya N.,
 Nishio T., Okada M., Plessy C., Shibusawa K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watahiki A., Okamura-Ohno Y., Suzuki H.,
 Hayashizaki Y.;
 "The transcriptional landscape of the mammalian genome.";
 Science 309:1559-1563 (2005).
 RN [3]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 PubMed=16141073; DOI=10.1126/science.1112009;
 RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 "Antisense transcription in the mammalian transcriptome.";
 Science 309:1564-1566 (2005).
 RN [4]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 PubMed=123354683; PubMed=12466851; DOI=10.1038/nature01266;
 Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzu H., Yamataka I., Kyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Balarew H., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
 Blake J.A., Bradt D., Brusic V., Chothia C., Corbani A., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,
- RA RA Grimmmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kuroochkin I.Y., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Peretea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reid D.J., Reid J.C., Reed J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimoda K., Sultan R., Takemoto Y., Taylor M.S., Tessdale R.D., Tonita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watansab Y., Wells C., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Wilming L.G., Wynshaw-Boris A., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hiraoka T., Hashizume W., Imotani K., Ishii Y., Itaya T., Kagaawa I., Miyauchi A., Sakai K., Sasaki D., Hayashizaki Y., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., RT "Analysis of the mouse transcriptome based on functional annotation of the mouse transcriptome based on functional annotation of cDNAs."
 RT 60,770 full-length cDNAs.";
 RT RN 420:563-573 (2002).
 RN [5]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 MEDLINE=2105660; PubMed=12171751; DOI=10.1038/35055500;
 RX RC RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Kawai T., Hara A., Iwasa M., Nishi K., Kiyoysawa H., Kondo S., Kondo A., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kado K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Steaibhi F., Suruki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bonaldo M.J., Built C., Fletcher C., Fujita M., Caribaldi M., Gustincich S., Hill D., Holmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P., Nordhoff P., Ring B., Ringwald M., Rodriguez J., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibusawa Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Kojtsuki S., Hayashizaki Y., RT "Functional annotation of a full-length mouse cDNA collection.";
 RT RN Nature 409:685-690 (2001).
 RN [6]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus; STRAIN=C57BL/6J;
 MEDLINE=20499374; PubMed=1042159; DOI=10.1101/gr.145100;
 RX RC RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Iwasa M., Ohara E., Watahiki K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai M., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RT "RIKEN integrated sequence analysis (RISA) system-324-Format sequencing pipeline with 324 multicapillary sequencer.";
 RT RN Genome Res. 10:1757-1771 (2000).
 RN [7]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=Bone marrow, and Thymus;
 MEDLINE=123354683; PubMed=12466851; DOI=10.1038/nature01266;
 RG RG RG RT RT RN RIKEN integrated sequence analysis (RISA) system-324-Format sequencing pipeline with 324 multicapillary sequencer.";
 RN RN RIKEN integrated sequence analysis (RISA) system-324-Format sequencing pipeline with 324 multicapillary sequencer.";
 RN RN RIKEN integrated sequence analysis (RISA) system-324-Format sequencing pipeline with 324 multicapillary sequencer.";

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| Hayashida K., Hayatsu N., Hiramoto K., Hirozane T., | QY | 409 | QYRDRLVVSGSSDNNTIRLWDIIGACRLVLEGEHLVRCDENKRIVSGAYDKIKYW | 468 |
| Hori F., Imotani I., Ishii Y., Itoh M., Kagawa I., Kasukawa T., | QY | 410 | QYRDRLVVSGSSDNNTIRLWDIIGACRLVLEGEHLVRCDENKRIVSGAYDKIKYW | 469 |
| Katoh H., Kawai J., Kojima K., Kondo S., Konno H., Koya S., | DB | 396 | QYRDRLVVSGSSDNNTIRLWDIIGACRLVLEGEHLVRCDENKRIVSGAYDKIKYW | 455 |
| Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., | DB | 11-OCT-2005 | integrated into UniProtKB/TriEMBL. | 455 |
| Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., | QY | 469 | DQLQALDPRAPASTLCLRTLVEHSGRVFRQFDEFQISSLSSHDDTDLIWDFLNVPSAQN | 528 |
| Saito R., Saithoh H., Sakai C., Sakai K., Sakizume N., Sano H., | DB | 07-FEB-2006 | entry version 6. | 515 |
| Sasaki D., Shibusawa K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., | QY | 456 | DQLQALDPRAPASTLCLRTLVEHSGRVFRQFDEFQISSLSSHDDTDLIWDFLNVPSAQN | 515 |
| Tagawa A., Takahashi F., Takaku-Akahira S., Tomaru A., Toyama T., Yasunishi A., Muramatsu M., Hayashi Y., Tomaru A., submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. | QY | 529 | ETRSPSRPTYTYSR | 542 |
| RL [9] | DB | 516 | ETRSPSRPTYTYSR | 529 |
| RN | RP | RESULT 6 | | |
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| RA | RP | DT 11-OCT-2005 | | |
| RA | RP | DT 11-OCT-2005, sequence version 1. | | |
| RC | RC | DT 07-FEB-2006, entry version 6. | | |
| RA | RA | STRAIN=CSFB/L61; TISSUE=Bone marrow; | | |
| RA | RA | Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., | | |
| RA | RA | Hori F., Iida J., Immura K., Imotani K., Itoh M., Kanegawa S., | | |
| RA | RA | Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., | | |
| RA | RA | Nishiyori H., Nomura M., Sakizume N., Sano H., Sasaki D., | | |
| RA | RA | Shibusawa K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanuki A., | | |
| RA | RA | Muramatsu M., Hayashizaki Y., submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. | | |
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| CC | CC | Distributed under the Creative Commons Attribution-NoDerivs License | | |
| CC | CC | ----- | | |
| DR | DR | NUCLEOTIDE SEQUENCE. | | |
| EMBL; AK041532; BAC0975.1.; mRNA. | DR | EMBL; AL669844; CA25519.1.; Genomic DNA. | | |
| EMBL; AL669951; CA166951.1.; JOINED: Genomic DNA. | DR | EMBL; AL669951; CA16698.1.; Genomic DNA. | | |
| EMBL; AL669844; CA16698.1.; JOINED: Genomic DNA. | DR | EMBL; AL669844; CA26098.1.; JOINED: Genomic DNA. | | |
| EMBL; AK152181; BAE13102.1.; mRNA. | DR | EMBL; AK152181; BAE13102.1.; mRNA. | | |
| HSSP; Q91297; IP22. | DR | Ensembl; ENSMUSG000000020271; Mus musculus. | | |
| DR | CC | Query Match Score 92.6%; Best Local Similarity 92.4%; Matches 512; Conservative 4; Indels 37; Gaps 4; | | |
| DR | CC | -----PR-SLWUGANLYVESMCALSQMSMPVSYRCL 48 | | |
| DR | CC | 1 MEPDSTEDIKTELM-CSV-----PR-SLWUGANLYVESMCALSQMSMPVSYRCL 48 | | |
| DR | Db | 1 MEPDSTEDIKTELMNTSVMQDNEDESPKSALW-----35 | | |
| DR | Db | 1 MEPDSTEDIKTELMNTSVMQDNEDESPKSALW-----35 | | |
| DR | QY | 49 QISNGTSSVIVSRKRPSSEGTYKEKDOLCIKYFDQWSSESDQVEFVEHLLISMCHYQHGHIN 108 | | |
| DR | QY | 36 QISNGTSSVIVSRKRPSSEGTYKEKDOLCIKYFDQWSSESDQVEFVEHLLISMCHYQHGHIN 95 | | |
| DR | QY | 109 SYLKPKMLQRDFTALPEQGLDHAENILSYLDARSCLAAELVCKENQVRVISFGMLWKLI 168 | | |
| DR | QY | 96 SYLKPKMLQRDFTALPEQGLDHAENILSYLDARSCLAAELVCKENQVRVISFGMLWKLI 155 | | |
| DR | QY | 169 ERMVRTDPLWKGLSERGMDOYLFKNRPTDGPNSPFYSLPKIIQDIEIESNWRCGRH 228 | | |
| DR | QY | 156 ERMVRTDPLWKGLSERGMDOYLFKNRPTDGPNSPFYSLPKIIQDIEIESNWRCGRH 215 | | |
| DR | QY | 229 NLQRIOCRESNSKGVYCYQDDEKEIISGLRDSNIKIMDKTSLECLKVLTGHTGSVLCLQY 288 | | |
| DR | QY | 216 NLQRIOCRESNSKGVYCYQDDEKEIISGLRDSNIKIMDKTSLECLKVLTGHTGSVLCLQY 275 | | |
| DR | QY | 289 DERIVTGSDSTVRWDVNGEVNLHNEAHLRFSGLMTCSRSIAWMDA 348 | | |
| DR | QY | 276 DERIVTGSDSTVRWDVNGEVNLHNEAHLRFSGLMTCSRSIAWMDA 335 | | |
| DR | QY | 349 SATDTLRLRVYGHRAVNVDFFDKYIVASGDRTKIVWSTSTCEFRVLNGHKGTCAC 408 | | |
| DR | QY | 336 SATDITLRVYGHRAVNVDFFDKYIVASGDRTKIVWSTSTCEFRVLNGHKGTCAC 395 | | |

RA	Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shiraki T., Suzuki S., Tagami M., Waki K., Watanuki A., Okamura-Ohno Y., Suzuki H., Kawai J., Hayashizaki Y., "The transcriptional landscape of the mammalian genome." ; Science 309:1559-1563 (2005). [3]	RA	TISSUE=Mammary gland; MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100; RX
RA	RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense transcription in the Mammalian Transcriptome." ; Science 309:1564-1566(2005). [4]	RA	RX
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H., Yagi K., Tomaru Y., Nogami Y., Nogami Y., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Blake J., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani A., Matsuda H., Batalov S., Beisel K.W., Gaasterland T., Gariboldi M., Gissi C., Forrest A., Frazer K.S., Grimmond S., Gustincich S., Hiraoka N., Jackson J.I., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malatis L., Marchionni L., Miki H., Nagashima T., Numata K., Okido T., Pavani W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reid J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Waranab Y., Wells C., Wilming L.G., Wynshaw-Boris A., Zimmer R., Hayatsu N., Yano T., Yuan Z., Zayylan M., Zhu Y., Zimmer P., Hayatsu N., Hayatsu N., Hirzaneh Kishikawa T., Komio H., Nakamura M., Sekizume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Watersston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." ; Nature 420:563-573 (2002). [5]	RA	RX
RA	NUCLEOTIDE SEQUENCE; TISSUE=Mammary gland; PubMed=12466851; DOI=10.1038/nature01266; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense transcription in the Mammalian Transcriptome." ; Science 309:1564-1566(2005). [4]	RA	RX
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H., Yagi K., Tomaru Y., Nogami Y., Nogami Y., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Blake J., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani A., Matsuda H., Batalov S., Beisel K.W., Gaasterland T., Gariboldi M., Gissi C., Forrest A., Frazer K.S., Grimmond S., Gustincich S., Hiraoka N., Jackson J.I., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Malatis L., Marchionni L., Miki H., Nagashima T., Numata K., Okido T., Pavani W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reid J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Waranab Y., Wells C., Wilming L.G., Wynshaw-Boris A., Zimmer R., Hayatsu N., Yano T., Yuan Z., Zayylan M., Zhu Y., Zimmer P., Hayatsu N., Hayatsu N., Hirzaneh Kishikawa T., Komio H., Nakamura M., Sekizume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Watersston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." ; Nature 420:563-573 (2002). [5]	RA	RX
RA	NUCLEOTIDE SEQUENCE; TISSUE=Mammary gland; MEDLINE=2108566; PubMed=11217851; DOI=10.1038/35055500; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota H., Matsuda H.A., Asburner M., Batalov S., Casavant T., Fliegschmann W., Gaspari T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzatorta J., Nobaarts P., Nordone P., Ring B., Schoenbach C., Seva T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection." ; Nature 409:685-690(2001). [6]	RA	RX
RA	NUCLEOTIDE SEQUENCE; TISSUE=Mammary gland; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Carninci P., Konno H., Okazaki Y., Muranatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes." ; Genome Res. 10:1617-1630(2000). [7]	RA	RX
RA	NUCLEOTIDE SEQUENCE; TISSUE=Mammary gland; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Carninci P., Itoh M., Aiwa K., Nagao S., Sasai N., Carninci P., Konno H., Ariyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hashizume T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanuki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer." ; Genome Res. 10:1557-1571(2000). [8]	RA	RX
RA	NUCLEOTIDE SEQUENCE; TISSUE=Mammary gland; Carninci P., Fukuda S., Hashizume M., Hayashizaki K., RA	RA	RX
RA	Shibata K., Itoh M., Aiwa K., Nagao S., Sasai N., Carninci P., Konno H., Murata M., Nanomiva N., RA	RA	RX
RA	Hori F., Iida J., Imamura K., Itoh M., Kanagawa S., Carninci P., Konno H., Murata M., Nanomiva N., RA	RA	RX
RA	Kawai J., Kojima M., Nomura H., Murata M., Nanomiva N., Sano H., Sasaki D., Carninci P., Konno H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Carninci P., Konno H., Muramatsu M., Hayashizaki Y., Submittted (APR-2004) to the EMBL/GenBank/DBJ databases.	RA	RX
RA	CC	CC	CC
RA	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NonDerivs License	CC	CC
RA	DR	DR	DR
RA	MGI; MGID:2144023; FBxw11; mRNA.	DR	DR
RA	GO; GO:0006512; Pubiquitin cycle; IBA.	DR	DR
RA	InterPro; IPR01810; F-box.	DR	DR
RA	InterPro; IPR01680; WD40.	DR	DR
RA	Pfam; PF00645; F-box.	DR	DR
RA	PFam; PF00400; WD40.	DR	DR
RA	PRINTS; PR00320; PROTEINBRPT.	DR	DR
RA	PRODOM; PD000018; WD40.	DR	DR
RA	SMART; SM00256; F-box.	DR	DR
RA	SMART; SM00320; WD40.	DR	DR
RA	PROSITE; PS50181; FBOX.	DR	DR
RA	PROSITE; PS00678; WD_REPEATS_1.	DR	DR
RA	PROSITE; PS50092; WD_REPEATS_2.	DR	DR
RA	PROSITE; PS50294; WD_REPEATS_REGION_1.	DR	DR
RA	KW Repeat; UbI Conjugation Pathway; WD repeat.	DR	DR
RA	SEQUENCE 529 AA; 6079 MW; CE035C809824D472 CRC64;	SQ	SQ
RA	Query Match 92.5%; Score 2664.5%; DB 2; Length 529; Best Local Similarity 92.2%; Pred. No. 6.6e-189; Matches 51; Conservative 5; MisMatches 1; Indels 37; Gaps 4;	QY	1 MEPSVIEDKTIEM-CSV-----PR-SIWLGANLVSMCALSCQLSMSVRCI 48
RA	RA 1 MEPSVIEDKTIEM-CSV-----PR-SIWLGANLVSMCALSCQLSMSVRCI 48	Db	1 MEPSVIEDKTIEM-CSV-----PR-SIWLGANLVSMCALSCQLSMSVRCI 48
RA	RA 1 MEPSVIEDKTIEM-CSV-----PR-SIWLGANLVSMCALSCQLSMSVRCI 48	Db	1 MEPSVIEDKTIEM-CSV-----PR-SIWLGANLVSMCALSCQLSMSVRCI 48
RA	RA 49 QISNGTSSVIVSRKPSEBNYQEKDLCIKYFDWSESQVEFVHLISRMCYQGHIN 108	QY	49 QISNGTSSVIVSRKPSEBNYQEKDLCIKYFDWSESQVEFVHLISRMCYQGHIN 108
RA	RA 36 QISNGTSSVIVSRKPSEBNYQEKDLCIKYFDWSESQVEFVHLISRMCYQGHIN 95	Db	36 QISNGTSSVIVSRKPSEBNYQEKDLCIKYFDWSESQVEFVHLISRMCYQGHIN 95
RA	RA 109 SYLKPLMLQRDFITALPEOGLDHIAENILSYLDARSCLAAELVCKEWQRTYSEGMLWKLI 168	QY	109 SYLKPLMLQRDFITALPEOGLDHIAENILSYLDARSCLAAELVCKEWQRTYSEGMLWKLI 168
RA	RA 96 SYLKPLMLQRDFITALPEOGLDHIAENILSYLDARSCLAAELVCKEWQRTYSEGMLWKLI 155	Db	96 SYLKPLMLQRDFITALPEOGLDHIAENILSYLDARSCLAAELVCKEWQRTYSEGMLWKLI 155
RA	RA 169 ERMYTRDPFLWKGLSERRGMDQYLFKNRPTDGPNSFYRSLYPKIIQDIEETESMRGCRH 228	QY	169 ERMYTRDPFLWKGLSERRGMDQYLFKNRPTDGPNSFYRSLYPKIIQDIEETESMRGCRH 228
RA	RA 156 ERMYTRDPFLWKGLSERRGMDQYLFKNRPTDGPNSFYRSLYPKIIQDIEETESMRGCRH 215	Db	156 ERMYTRDPFLWKGLSERRGMDQYLFKNRPTDGPNSFYRSLYPKIIQDIEETESMRGCRH 215

RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Giuslini S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mazzarelli J., Mombretti P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Tato K., Schoenbach C., Seta Y., Shibusawa Y., Storch K.-F., Wynnshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.;	KW Repeat; Ub1 conjugation pathway; WD repeat.
RA	"Functional annotation of a full-length mouse cDNA collection.";	SQ SEQUENCE 508 AA; A048EFA4A78C550 CRC64;
RL	Nature 409:685-690(2001).	Query Match 92.4%; Score 2660; DB 2; Length 508; Best Local Similarity 93.4%; Pred. No. 1, 4e-188; Matches 506; Conservative 2; Mismatches 0; Indels 34; Gaps 1;
RN	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Kidney;	QY 1 MEPDSTVDEDKTIELMCSPVRSLWLGANLVEMSCALSCLOSMPSVRCLQISNGTSSIVS 60 DB 1 MEPDSTVDEDKTIELM-----ISNTSSIVS 26
RC	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Kidney; MEDLINE=2049374; PubMed=11042155; DOI=10.1101/gr.145100;	QY 61 RKRPSGEQNYQEKEKDCKYKFDQMSDOVEFVHLSRPMCHYOHGHINSYLKPMQLQRDFI 120 DB 27 RKEPSEGNYQEKEKDCKYKFDQMSDQEVFVHLSRPMCHYOHGHINSYLKPMQLQRDFI 86
RX	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subration of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";	QY 121 TALPEQGLDHIAENILSYLDARSCLAAELVCKEWQRVSEGMILWKLTERMYRTDPLWKG 180 DB 87 TALPEQGLDHIAENILSYLDARSCLAAELVCKEWQRVSEGMILWKLTERMYRTDPLWKG 146
RA	[7]	QY 181 LSERRGNDQYLFLKRNPTDGPNSFYRSLYPKIQDIEETESMRGRHNLQRQCRSENS 240 DB 147 LSERRGNDQYLFLKRNPTDGPNSFYRSLYPKIQDIEETESMRGRHNLQRQCRSENS 206
RA	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Kidney;	QY 241 KGYYCLOYDDEKKLISGLDNRNSIKIWDKTSLECLKVLTGHTGSVSLCLOYDERIVTVGSSDS 300 DB 207 KGYYCLOYDDEKKLISGLDNRNSIKIWDKTSLECLKVLTGHTGSVSLCLOYDERIVTVGSSDS 266
RA	Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishina T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexillary sequencer.";	QY 301 TVRVWDVNTGEVNTLTHNEAVHLRLRSNGLMVTSKDRSLAVWDMASATDTLRLVY 360 DB 267 TVRVWDVNTGEVNLNTLHHNEAVHLRLRSNGLMVTSKDRSLAVWDMASATDTLRLVY 326
RA	[8]	QY 361 GHRAAVNVYDFDDKCYIVSASGDRTIKWMSSTSTCEBFVTLNGHKGIACLQYDRLVVSS 420 DB 327 GHRAAVNVYDFDDKCYIVSASGDRTIKWMSSTSTCEBFVTLNGHKGIACLQYDRLVVSS 386
RA	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J; TISSUE=Kidney;	QY 421 SDNTIRLMDIECGACLRVLEGHRELVRVRCIREFDNKRVSGAYDGSKIKWDLQALDPRAPA 480 DB 387 SDNTIRLMDIECGACLRVLEGHRELVRVRCIREFDNKRVSGAYDGSKIKWDLQALDPRAPA 446
RA	Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Koijima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno H., Murata M., Nakamura M., Ninomiya N., Shirata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	QY 481 STLCRLTVEHSGRVFRQLQDEFQIISSSHDDTLLWDFLNVPSPQAQNTRSSRTRYI 540 DB 447 STLCRLTVEHSGRVFRQLQDEFQIISSSHDDTLLWDFLNVPSPQAQNTRSSRTRYI 506
RA	[9]	QY 541 SR 542 DB 507 SR 508
RP	NUCLEOTIDE SEQUENCE. STRAIN=C57BL/6J;	RESULT 8
RA	Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Koijima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno H., Murata M., Nakamura M., Ninomiya N., Shirata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	OS Mus musculus (Mouse). OC Name=Fbxw1; Synonyms=Fbxw1b, mkIA00696; OC Nucleotide sequence.
CC	Copyrighted by the UniProt Consortium. see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License	NCBI_TaxID=10090; RN [1]; RP TISSUE=brain; Metazoa; RC Chordata; Craniata; Vertebrata; Euteleostomi; RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T., Sciurognathus; RA Ohara O., Koga H.; Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
DR	EML; AK168667; BB40519.1; -; mRNA. EMBL; AK10086; BB35617.1; -; mRNA. GO; GO:0006512; Pubiquitin cycle; IEA. InterPro; IPR001810; F-box. InterPro; IPR001680; WD40. Pfam; PF00646; F-box; 1. Pfam; PF00400; WD40; 7. PRINTS; PRO0320; GPOTEINBRPR. PRODOM; BD000018; WD40; 4. SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7. PROSITE; PS50181; FBOX; 1. PROSITE; PS00678; WD_REPEATS_1; 5. PROSITE; PS50082; WD_REPEATS_2; 7. PROSITE; PS50294; WD_REPEATS_REGION; 1.	RA Copyright by the UniProt Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerivs License CC EMBL; AB093260; BAC41444.1; -; mRNA.

			Query Match Score 85.0%; Best Local Similarity 86.1%; Pred. No. 7e-173; Matches 466; Conservative 30; Missmatches 26; Index 19; Gaps 4;
Db	456 DLQALDPPAPASTLCLRTLVHSGRVFFLQFQIISSHDDTILWDFLNVPPSSAPN	515	
Qy	529 ETTRSPSRITYISR	542	
Db	516 ETRSSPSRITYISR	529	
RESULT 10	Q6PGW4 BRAE BRARE PRELIMINARY; PRT; 527 AA.		
ID	O6PGW4;		
AC	Q6PGW4;		
DT	05-JUL-2004, integrated into UniProtKB/TREMBL.		
DT	05-JUL-2004, sequence version 1.		
DT	07-FEB-2006, entry version 17.		
DE	ZGC:63728.		
GN	Brachydanio rerio (Zebrafish) (Danio rerio).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopercygi; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.		
OC			
OC			
OX	NCBI_TaxID=7955;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=AB; TISSUE=Whole body;		
RA	MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausberg R.L., Colins F.S., Wagner L., Schaefer C.M., Schulier G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bozak S.A., McEwan P.J., McErlean K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimes J.W., Schnitz J., Myers R.M., Butterfield Y.F.N., Krzywinski M.I., Skalska U., Smailus D.E., Schenck A., Schein J.E., Jones S.J.M., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=AB; TISSUE=Whole body;		
RA	Strausberg R.; Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.		
CC	Copyright by the UniProt Consortium see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License		
CC	Ensembl; ENSDARG000000017230; Danio rerio.		
DR	BC056809; ARH56809; -; mRNA.		
DR	ZFIN; ZFIN-ID-0426-0426-0426; Danio rerio.		
DR	GO:0006512; Pubiquitin cycle; IEA.		
DR	InterPro; IPR00180; F-box.		
DR	InterPro; IPR00180; WD repeat domain.		
DR	Pfam; PF00646; F-box; 1.		
DR	PFAM; PF00400; WD0; 7.		
DR	PRINTS; PR00320; GPROTEINBPR1.		
DR	ProDom; PD000018; WD40; 4.		
DR	SMART; SM00256; FBOX; 1.		
DR	SMART; SM00320; WD0; 7.		
DR	PROSITE; PS50181; FBOX; 1.		
DR	PROSITE; PS50678; WD_REPEATS_1; 5.		
DR	PROSITE; PS50082; WD_REPEATS_2; 7.		
DR	PROSITE; PS50394; WD_REPEATS_REGION; 1.		
KW	Repeat; Ubiquitination Pathway; WD repeat.		
SEQUENCE	527 AA; 60547 MW; 5633FC014CA099C3 CRC64;		
RA	Deember 10		

- RA Thomas D., Strebel K., Benarous R.;
RT "A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu
connects CD4 to the ER degradation pathway through an F-box motif.";
Mol. Cell 1:555-574 (1998).

[3] RN NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2).
MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;

RX Cenciarelli C., Chiari D.S., Guardavaccaro D., Parks W., Vidal M.,
RA "Identification of family of human F-box proteins.";
Curr. Biol. 9:1177-1179 (1999).

[4] RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RP TISSUE=Brain;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauschuk S.D., Collins P.S., Wagner L., Shanmen G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Matsuyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McErlean K.J., Malek J.A., Gundarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergreen B.J., Lu X., Gibbs R.A.,
RA Fahey J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Dickson M.C.,
RA Rodriguez A.C., Grzimek J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smilus D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marrs M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[5] RN RP CHARACTERIZATION.
RX MEDLINE=99145464; PubMed=9990852;

RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TrCP)-ubiquitin ligase complex associates specifically
RT with the phosphorylated destruction motifs in I-kappa-B-alphal and beta-
catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
Genes Dev. 13:270-283 (1999).

[6] RN RP INTERACTION WITH UBQLN1.
RC TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;

RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersha N.L., Gill G., Howley P.M.,
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RT Mol. Cell 6:409-419 (2000).

[7] RN RP INTERACTION WITH PHOSPHORYLATED CTNNB1.
RX MEDLINE=2072105; PubMed=12077367;

RA Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Landau Z.,
RA Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells";
RT J. Cell Sci. 115:2771-2780 (2002).

[8] RN X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=2206071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;

RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-Trcp1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-Trcp1) ubiquitin
RT ligase.";
RT Mol. Cell 11:1445-1456 (2003).

-1- BOX PROTEIN) ubiquitin ligase complex, which mediates the

FT	HELIx	224	234	234	Qy	538	TYISR	542
FT	TURN	234	235	235	Db	601	TYISR	605
FT	STRAND	235	237	244				
FT	HELIx	237	244	247				
FT	STRAND	245	248	251				
FT	HELIx	248	251	265				
FT	STRAND	265	266	285				
FT	HELIx	266	285	288				
FT	TURN	286	288	296				
FT	STRAND	296	297	301				
FT	HELIx	297	301	302				
FT	STRAND	306	306	310				
FT	STRAND	313	313	323				
FT	HELIx	313	323	325				
FT	STRAND	325	332	332				
FT	TURN	335	339	339				
FT	STRAND	343	344	344				
FT	STRAND	346	350	350				
FT	STRAND	353	360	360				
FT	TURN	361	362	362				
FT	STRAND	363	363	363				
FT	STRAND	365	372	372				
FT	STRAND	375	379	379				
FT	STRAND	384	384	384				
FT	STRAND	386	390	390				
FT	TURN	393	394	394				
FT	STRAND	395	400	400				
FT	TURN	401	402	402				
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Db	1 MEP-DSVIEDKTIBLMCSVPRSLMIGCANLVEENCALSLC----- 39							
Qy	1 MDPAEAVLGSKAKFMCMSPRSLMIGCSSLADMSPLRQLYNPGTGAFTQNSSEREDC 60							
Db	40 -----QSPMPSTVCL----- 39							
Qy	1 SRKRPSEGVNYQEKEKDLCITYFDQYSESDOYEVHLISRMCHYQHGHINSYLPKMLQDFP 119							
Db	121 PKQRKLSSAYEKERELCVCYTFEQYSESDQYEVHLISRMCHYQHGHINSYLPKMLQDFP 180							
Qy	120 ITALPEQGDHIAINLSTLDARSICAAELVKREWQYRVSSEGMLWKQKLIERMVRTDPLMK 179							
Db	181 ITALPARGDHLIAENLSTLDASKLCAALVKEWYRTSDGMLWKQKLIERMVRTDLSMR 240							
Qy	180 GLSERRGWDQYLFKNRPTDQ- PPNFSYRSLPKIIDIETIESNWRCGRHNLRQIQCWS 237							
Db	241 GLAERRGWQYLFKNPKPPDGNAPPNSFYALPKIIDIETIESNWRCGRHSQRIHCRS 300							
Qy	238 ENSKCVYCYQYDDEKISGLRDSIKIWMDTSLECLKVLTGHFCSVLCLQYDERRVITG 297							
Db	301 ETSKGVYCLQYDDQKIVSGURDNNTIKIWMDTLECLKVLTGHFCSVLCLQYDERRVITG 360							
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Db	361 SDSTYRVWDNTGMINTLHHCEAVLHIFNGMMVTCSKRSIAWMASAPTDITLRR 420							
Qy	358 VLVGHRAANVVDFFDKYIVSASGDRTIKWSTCEFFRTLACHKGIACLQYDRRLVV 417							
Db	422 VLVGRAANVVDFFDKYIVSASGRTIKWNTSTCEFFRTLACHKGIACLQYDRRLVV 480							
Qy	418 SGSSDNTIRLWIDEGACRVLGEHEELJRCIREDFDNKRIVSGAYDGKIKWMDQALDPR 477							
Db	481 SGSSDNTIRLWIDEGACRVLGEHEELJRCIREDFDNKRIVSGAYDGKIKWMDLVAAFLDR 540							
Qy	478 APASTLCLRLVENVSGRVRFLQDFQISSSHDTILWDFLNVPSONETRSPSRVY 537							
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 RA Georgii-Hemming P., Gineras T.R., Gojobori T., Green R.E.,
 RA Harbers M., Hayashi A., Hensh K., Hirokawa N.,
 RA Hill D., Humirecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kaito H., Kollia S.P., Krushan A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau D.F., Lazarev M., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madeira M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone P., Miyake S., Morris K.,
 RA Motaguchi-Tabor S., Mulder N., Nakuchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavon W.J., Pavesi G.,
 RA Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rose B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seino S., Sesia L., Sheng Y.,
 RA Shiba Y., Shimada H., Shinada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiyama K., Sultan R., Takenaka Y., Takai K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nieuwen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamamoto H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Matrick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawai J., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanuki A., Okamura-Ohno Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.:
 RT "The transcriptional landscape of the mammalian genome.";
 RN [4] STRAIN=C57BL/6J;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RN [3] NUCLEOTIDE SEQUENCE.
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 (Genome Network Core Team) and the FANTOM Consortium;
 RG "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1559-1563 (2005).
 RN [4] STRAIN=C57BL/6J;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Mogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.A., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradd D., Chothia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A.R., Frazer K.S.,
 RA Gaasterland T., Garibaldi M., Giassi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa Y., Jackson J.I., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Magiott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavon J.U., Partea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Rees J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultan R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang J., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shiba T., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RNA full-length cDNAs.";
 RN [5] NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J;
- Db 120 ITALPEOGDHAENILSYLDRSILCAEVLCKEWVRISEGMILWKKLIERMVRDPFLWK 179
 RA CARNICINI P., HAYASHIZAKI Y.;
 DT 11-OCT-2005, integrated into UniProtKB/TREMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
- DE Blastocyt library enriched library, RIKEN full-length enriched library,
 DE clone:11C0023nJ12 product:beta-transducin repeat containing protein,
 DE full insert sequence.
- GN Name=trc;
- OS Mus musculus (Mouse)
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- OC Mammalia; Muridae; Murinae; Mus.
- NCBI_TAXID=10050;
- OX RN [1] NUCLEOTIDE SEQUENCE.
- Db 121 TYISR 542
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 RN [3] NUCLEOTIDE SEQUENCE.
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 AC Q3ULIA2;
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
- DE Blastocyt library enriched library, RIKEN full-length enriched library,
 DE clone:11C0023nJ12 product:beta-transducin repeat containing protein,
 DE full insert sequence.
- GN Name=trc;
- OS Mus musculus (Mouse)
- OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- OC Mammalia; Muridae; Murinae; Mus.
- NCBI_TAXID=10050;
- OX RN [1] NUCLEOTIDE SEQUENCE.
- Db 122 TYISR 542
 RN [2] TYISR 605
 RN [3] NUCLEOTIDE SEQUENCE.
- STRAIN=C57BL/6J;
- RX MEDLINE=997923; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA RT "High-efficiency full-length cDNA cloning.";
 RA RL Methods Enzymol. 303:19-44 (1999).
- RP NUCLEOTIDE SEQUENCE.
- RC PubMed=16141072;
- RA CARNICINI P., KASUKAWA T., KATAYAMA S., GOUGH J., FRITH M.C., MAEDA N.,
 RA OYAMA R., RAVASI T., LENHARD B., WELLS C., KODISI R., SHIMOKAWA K.,
 RA BAJIC V.B., BRENNER S.E., BARALOV S., FORREST A.R., ZAVOLAN M.,
 RA DAVIS M.J., WIMING L.G., AIDINIS V., ALLEN J.E.,
 RA AMBESI-IMPLUMBATI A., APWEILER R., ATARUJI R.N., BAILEY T.L.,
 RA BANSAL M., BAXTER L., BEISEL K.W., BERSANO T., BONO H., CHALK A.M.,
 RA CHIU K.P., CHOUDHARY V., CHRISTOFFELS A., CLUTTERBUCK D.R.,
 RA CROWE M.L., DALLA E., DAIRYMPLE B.P., DE BONO B., DELLA GATTA G.,
 RA DAVIS D., DOWN T., ENGSTROM P., FAGIOLINI M., FAULKNER G.,
 RA FLETCHER C.F., FUKUSHIMA T., FURUNO M., GARIOLDI M.,
 RA

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;	DR PROSITE; PS50181; FBOX; 1.
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	DR PROSITE; PS00678; WD_REPEATS_1;
RA Arakawa T., Hara P., Nishii K., Kiyosawa H., Adachi J., Fukuda S.,	DR PROSITE; PS00822; WD_REPEATS_2;
RA Aizawa K., Izawa M., Kondo S., Yamanaka I., Saito R.,	DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	KW Repeat; Ubl_onjugation_pathway; WD repeat.
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,	SEQUENCE 605 AA; 68942 MW; 557B3942F52DC472 CRC64;
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,	
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,	Query Match 84.7%; Score 2437 5; DB 2; Length 605;
RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,	Best Local Similarity 75.4%; Pred. No. 5.5e-12;
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	Matches 456; Conservative 51; Mismatches 35; Index 63; Gaps 4;
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	Qy 1 MBP-DSVDEDKTEILMCSVPRIWLGCANLVSMSMCALSCL-----
RA Lyons P., Marchionni L., Mazzarelli J., Mazzarelli P.,	Db 1 MDPAEVAVLOEKALKFMCSMPRSIWLGOSSLAISMPSLRCLYNPGTGALTAFONSEREDC 60
RA Nordone P., Ring B., Ringewald M., Rodriguez I., Sakamoto N.,	40 -----
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,	Qy -----QSMPSPVRL--QINGTSSVIV 59
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,	Db 61 NNGBPSPKLIPEKNSLRTOTYNSCARLGINQETVCLSTAMKTENCVAKAKLANGTSSMIV 120
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,	
RA Hayashizaki Y.;	Qy 60 SRKRPSSEGNYQEKDLCTKYFDOWSSESPQVEFHLLSRMCHYQGHINSYLPKPMQRDF 119
RT "Functional annotation of a full-length mouse cDNA collection.";	Db 121 PKORKLSSAYEKEKELCYKFBWSSESQVEFHLLSQMCYQGHINSYLPKPMQRDF 180
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RC STRAIN=C57BL/6J;	Qy 120 ITALPEQCDLHAENILSYLDARSLSLAAELVCKEMQVRVISEGMLWKKLIERMVRTDPLWK 179
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;	Db 181 ITALPARSGIDHIAENILSYLDASKLAAELVCKEWYVTSQDMWLKKLIERMVRTDSIWR 240
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,	
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,	Qy 180 GLSERGRWDQYLIFPKNRPTD--GPNPSFYSRLSPYKIQDIEITESWNWGRHNLQRICRS 237
RA "Normalization and subtraction of cap-trap-selected cDNAs to	Db 241 GLAERGRWGQYLEKPKPDENAPPNSFYRALPKIQDIETESWNWGRHSQLRICRS 300
RT prepare full-length cDNA libraries for rapid discovery of new genes.";	
RT Genome Res. 10:1617-1630 (2000).	Qy 238 ENSKGVYCLQYDDEKILISGLRDNSTIKWDTKSLECLKVLGTHTGSVLCLOYDERIVVTGS 297
RN [7]	Db 301 ETSGKGVYCLQYDQKIVGLDRNTIKWDTKSLECLKVLGTHTGSVLCLOYDERIVVTGS 360
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=C57BL/6J;	Qy 298 SDSTVRWVDNTGEVBLNTLHNEAVMLRFNSGLMYTCSKDSRISAVDMASATDTLRR 357
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,	Db 361 SDSTVRWVDNAGEMMLNLHICAEVHLRFENGMYTCSKDSRISAVDMASPTDTLRR 420
RA Konno H., Itoh M., Nishimura J., Nishimura S., Hizama M., Nishina T., Harada A.,	
RA Sumi N., Ishii Y., Nishimura S., Hizama M., Nishina T., Harada A.,	Qy 358 VLVGHRRAAVNWVDDFDKYIVSAGDRITKWSSTCCEPVRTLNGHREGIACLYQRDLVV 417
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,	Db 421 VLVGHRRAAVNWVDDFDKYIVSAGSDRTIKWNTSTCCEPVRTLNGHREGIACLYQRDLVV 480
RA Fujisawa S., Inoue K., Ogawa T., Ohara M., Ohara E., Watanuki M.,	
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,	Qy 418 SGSSDNTIRLWLDIEGACIARLVEGHHEELVRCFIRKRVSGAYGKIKWVDIQLADDPR 477
RA Okezaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,	Db 481 SGSSDNTIRLWLDIEGACIARLVEGHHEELVRCFIRKRVSGAYGKIKWVDIQLADDPR 540
RA "RIKEN integrated sequence analysis (RISA) system-384-format	
RT sequencing pipeline with 384 multicapillary sequencer.";	CC Copyrighted by the UniProt Consortium. see http://www.uniprot.org/terms
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.	Distributed under the Creative Commons Attribution-NoDerivs License
RN [8]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=C57BL/6J;	Qy 478 APASTLCLRLTYVHSGRVFRLOQDEFQTISSHHDDTILWDFINPPSAQNETRSPSRTY 537
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,	DR ID Q571K6_MOUSE PRELIMINARY; PRT; 639 AA.
RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,	AC AC Q571K6_
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,	DT DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
RA Nishiyori H., Nomura H., Ohno M., Sakizume N., Sano H., Sasaki D.,	DR GO; GO:0006511; Protein-conjugating enzyme activity; RCA.
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanuki A.,	DR GO; GO:0006464; Ubiquitin modifying enzyme activity; RCA.
RA Muramatsu M., Hayashizaki Y.;	DR GO; GO:0007165; Ubiquitin conjugation; RCA.
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.	DR InterPro; IPR001810; F-box.
CC Copyrighted by the UniProt Consortium. see http://www.uniprot.org/terms	DR InterPro; IPR001680; WD40.
CC Distributed under the Creative Commons Attribution-NoDerivs License	DR Pfam; PF00646; F-box; 1.
CC EMBL; ALKB634; BE26547; 1; - mRNA.	DR Prints; PR00320; PROTEINBPRPT.
CC MGII; MGII; 18871; BTRC.	DR Prodrom; PD000018; WD40; 4.
CC GO; GO:0005783; C-endoplasmic reticulum; RCA.	DR SMART; SM00256; Fbox; 1.
CC GO; GO:0004840; Ubiquitin conjugating enzyme activity; RCA.	DR SMART; SM00320; WD40; 7.
CC GO; GO:0006464; Ubiquitin modifying enzyme activity; RCA.	DR RN [1] _TaxID=10090;
CC GO; GO:0007165; Ubiquitin transduction; RCA.	RC NUCLEOTIDE SEQUENCE.
CC InterPro; IPR001810; F-box.	OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
CC InterPro; IPR001680; WD40.	OC Muroidea; Muridae; Murinae; Mus.
CC Pfam; PF00446; F-box; 1.	OC Muroidea; Eutheria; Buauchontogires; Glires; Rodentia; Sciurognathi;
CC Prints; PR00320; PROTEINBPRPT.	OX NCBI_TaxID=10090;
CC Prodrom; PD000018; WD40; 4.	RP TISSUE=Brain;
CC SMART; SM00256; Fbox; 1.	
CC SMART; SM00320; WD40; 7.	

RA	Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Nagase T., Ohara O., Koga H.; "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene."	Qy	478 APASTLCLRLTVEHSSGRVFRQLQFQIISSSHDDTLWIDFLNVPSSAQNETRSPSRTY 537
RT	The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs Identified by Screening of terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries,";	Db	575 APAGTLCRLTVEHSSGRVFRQLQFQIIVSSSHDDTLWIDFLNVPSSAQNETRSPSRTY 634
RT	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.	Qy	538 TYISR 542
RL		Db	635 TYISR 639
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	EMBL; AK220183; BAD9368.1; - mRNA.		RESULT 15
DR	Ensembl; ENSMUSG00000025217; Mus musculus.	Q68DSO HUMAN	Q68DSO HUMAN PRELIMINARY; PRT; 564 AA.
DR	MGI; MGID:133871; Drtc.	ID	Q68DSO_HUMAN
DR	GO; GO:0005783; C: endoplasmic reticulum; RCA.	AC	Q68DSO;
DR	GO; GO:0004840; F: ubiquitin conjugating enzyme activity; RCA.	DT	11-OCT-2004, integrated into UniprotKB/TREMBL.
DR	GO; GO:0006464; P: protein modification; RCA.	DT	11-OCT-2004, sequence version 1.
DR	GO; GO:0007165; P: signal transduction; RCA.	DT	07-FEB-2006, entry version 11.
DR	GO; GO:0006511; P: ubiquitin-dependent protein catabolism; RCA.	DE	Hypothetical protein DKFP781N011.
DR	InterPro; IPR00180; F-box.	GN	Name=DKFP781N011;
DR	InterPro; IPR00180; F-box.	OS	Homosapiens (Human).
DR	Pfam; PF00646; F-box; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
DR	Pfam; PF00400; WD40; 7.	OC	OC
DR	PRINTS; PRO0320; GPROTEINBPT.	RN	[1] _TaxID=9606;
DR	SMART; SM00256; FBOX; 1.	RP	NUCLEOTIDE SEQUENCE.
DR	PROSITE; PS50181; FBOX; 1.	RC	TISSUE=Amygdala;
DR	PROSITE; PS00678; WD_REPEATS_1; 6.	RG	The German cDNA Consortium;
DR	PROSITE; PS00083; WD_REPEATS_2; 7.	RA	Koehler K., Beyer A., Meves H.W., Weil B., Osanger A.,
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.	RA	Fobo G., Han M., Wiemann S.;
KW	WD repeat.	RL	Submitted (AUG-2004) to the EMBL/GenBank/DDJB databases.
FT	NON_TER 1	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
SO	SEQUENCE 639 AA; 72569 MW; C53D41E9A732575 CRC64;	CC	Distributed under the Creative Commons Attribution-NoDerivs License
Query Match	84.6%; Score 2436.5; DB 2; Length 639;	CC	
Best Local Similarity	75.4%; Pred. No. 7e-172;	DR	EMBL; CR749295; CAH18150.1; - mRNA.
Matches 456; Conservative	50; Mismatches 36; Indels 63; Gaps 4;	DR	Ensembl; ENSG00000166167; Homo sapiens.
Db	1 MEP-DSVIEDKTELMSVPRSLWLGCANLYVESMCAL-CL-----39	DR	DR
Qy	1 : : : : : : : : : : : : : : : : : : :	DR	DR
Db	35 MDPAEAVLQEALKFMSMPKSLWLGSLSADSMSPLRCLYNPGTGALITAQNSSERDC 94	DR	InterPro; IPRO01680; WD40.
Qy	40 -----	DR	PF006512; P: ubiquitin cycle; IEA.
Db	95 NNGEPPKKIIPERNSLRQTYNSCARLICINQETVCLTSTAMKTCYAKIANGTSSMIV 154	DR	InterPro; IPRO01810; F-box.
Qy	60 SRKPSEGVNYQKEKDLCKYQFQWSESDQVEFVHLISRMCFQKDPQWVQKDFQWVQKDFQWVQDF 119	DR	DR
Db	155 PKQRKLSASAYKEKEKELCKVCKYFQWSESDQVEFVHLISQMCHYQHGHINSVSLKPKMLQRFDF 214	DR	PROSITE; PS00678; WD_REPEATS_1;
Qy	120 ITALPEQGLDHIAENTILSYLDARSLSLCAELVKCWERVVISGMLWKLLIERMVRTDPLWK 179	DR	DR
Db	215 ITALPARGLWDYLKFKNRPTD-GPPNSFYSRSLPYKTIQDIETIESNWGRGHNLQTOCRS 237	DR	DR
Qy	180 GLSERGCGWDYLKFKNRPTD-GPPNSFYSRSLPYKTIQDIETIESNWGRGHNLQTOCRS 237	DR	DR
Db	275 GLAERKGCGWQYLFKNRPTD-GPPNSFYSRSLPYKTIQDIETIESNWGRGHNLQTOCRS 334	DR	DR
Qy	238 ENSKGVYCLQDDEKISGLRDNSIKIWDTKSLECLKLVTGTYLQDDEVITVG 297	DR	DR
Db	335 ETSKGVYCLQDQKIVSLGRDNTKIKWDKSTLECKRKLVTGTYLQDDEVITVG 394	DR	DR
Qy	298 SDSTVRWVDNTGEVINTLHNEAVHLRFNSNLAVNTSKDRSIAWDMASATDITLRR 357	Db	1 MCSPMSLWLGCSLADSMPSLRCYLNPGTCALTFQTYNQETVCLASTMK 60
Db	395 SDSTVRWVDNAGEMINTLHCEAVHLRFNSGMVNTSKDRSIAWDMASPTDITLRR 454	Qy	44 SVRCL -- QISNGTSSVIVSRKPSRGNYQKEKDLCKYFQDQWESSDQVEFVHLISRMCF 100
Qy	358 VLVGHRRAAVNTYDFDDKXIVSASGDRTKIVNSTSTCERFVRLTNGHKGIAQLYDRIVY 417	Db	61 TENCVAKTKLANGTSSMIVPKQRKLSASYKEKEKELCVKYFQWSESDQVEFVHLISQC 120
Db	455 VLVGHRRAAVNTYDFDDKXIVSASGDRTKIVNSTSTCERFVRLTNGHKGIAQLYDRIVY 514	Qy	101 HYQHGHINSVSLKPKMLORDFTALPEQGLDHIAENTILSYLDARSLSAELVKCWERVISE 160
Qy	418 SGSSDNTIRLWDIEGAGLRVLEGHEELVRCERFDNKRIVSAYDGKIKWDLQALDPR 477	Db	121 HYQHGHINSVSLKPKMLORDFTALPARGLDTIAENTILSYLDARSLSAELVKCWERVTS 180
Db	515 SGSSDNTIRLWDIEGAGLRVLEGHEELVRCERFDNKRIVSAYDGKIKWDLQALDPR 574	Qy	161 GMLWKLIERMVRTDPLWKGLSERGCGWDQYLFKNPRTDG--PPNCFYRSYLPKIQDIFT 218
Qy		Db	181 GMLWKLIERMVRTDLSWRGLAERGNGQYFLKNPDPGNAPNSFYRALYLPKIQDIFT 240

Qy	219	I E S N W R C G H N L O R I Q C R E S E N S K G V Y C I Q Y D D E K I S G I R D N S T I K I W D K T S L E C L K V L T G	278
Db	241	I E S N W R C G H S L Q I H C R E T S K V C L O Y D D Q I V S G I R D N T I K I W D K T S L E C L K V L T G	300
Qy	279	H T G S V U C L Q D Y D E R V I T G S S D S T R V W D V N T G E V I N T L I H N E A V L H I R F S N G L M V T C S K	338
Db	301.	H T G S V U C L Q D Y D E R V I T G S S D S T R V W D V N T G E M L N T L I H C B A V L H I R F N G M M V T C S K	360
Qy	339	D R S I A W D D A S P O T I L R R V L V G H R A A V N V D F D K Y I V S A G D R T I K W S T S C F V T	398
Db	361.	D R S I A W D D A S P O T I L R R V L V G H R A A V N V D F D K Y I V S A G D R T I K W N T S C F V T	420
Qy	399	L N G H K R G I A C L Q Y R D R L V Y V G S S D N T I R I W D I E C G A C I R V L E G H E E L V R C I R F D N K R I V S	458
Db	421	L N G H K R G I A C L Q Y R D R L V Y V G S S D N T I R I W D I E C G A C I R V L E G H E E L V R C I R F D N K R I V S	480
Qy	459	G A Y D G K I K W D L Q A A L D P R A P A S T I C I R T L V E H S G R V P L Q D E F Q I S S H D D T I I W D	518
Db	481	G A Y D G K I K W D L V A A L D P R A P A G T I C I R T L V E H S G R V P L Q D E F Q I V S S H D D T I I W D	540
Qy	519	F L N V P S A Q N E T R S P R S R T Y I S R	542
Db	541	F L N D P A A Q A E P P R S P R S R T Y I S R	564

Search completed: August 25, 2006, 07:22:29
 Job time : 307 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	2879	100.0	542	2	US-09-832-161-16	Sequence 16, Appli
2	2384.5	82.8	569	2	US-09-832-161-18	Sequence 18, Appli
3	2384.5	82.8	569	2	US-09-385-19A-2	Sequence 2, Appli
4	2384.5	82.8	569	2	US-09-601-168B-2	Sequence 2, Appli
5	2286.5	79.4	517	1	US-08-190-802A-10	Sequence 30, Appli
6	2286.5	79.4	517	2	US-08-473-089-30	Sequence 30, Appli
7	2286.5	79.4	517	2	US-08-487-072A-10	Sequence 30, Appli
8	643	22.3	626	2	US-09-213-088-21	Sequence 21, Appli
9	643	22.3	626	2	US-09-328-077D-21	Sequence 21, Appli
10	641.5	22.3	540	2	US-09-213-088-7	Sequence 7, Appli
11	641.5	22.3	540	2	US-09-213-088-10	Sequence 10, Appli
12	641.5	22.3	540	2	US-09-328-077D-7	Sequence 7, Appli
13	641.5	22.3	540	2	US-09-328-077D-10	Sequence 10, Appli
14	641.5	22.3	540	2	US-09-328-077D-10	Sequence 8, Appli
15	641.5	22.3	545	2	US-09-328-077D-6	Sequence 6, Appli
16	641.5	22.3	545	2	US-09-213-088-6	Sequence 6, Appli
17	641.5	22.3	553	2	US-09-213-088-5	Sequence 5, Appli
18	641.5	22.3	553	2	US-09-328-077D-5	Sequence 5, Appli
19	641.5	22.3	559	2	US-09-213-088-9	Sequence 9, Appli
20	641.5	22.3	559	2	US-09-328-077D-9	Sequence 9, Appli
21	641.5	22.3	589	2	US-09-213-088-8	Sequence 8, Appli
22	641.5	22.3	589	2	US-09-328-077D-8	Sequence 8, Appli
23	641.5	22.3	592	2	US-09-213-088-4	Sequence 4, Appli
24	641.5	22.3	592	2	US-09-328-077D-4	Sequence 4, Appli
25	641.5	22.3	627	2	US-09-213-088-3	Sequence 3, Appli
26	641.5	22.3	627	2	US-09-328-077D-3	Sequence 3, Appli

Qy 272 CLKVLTGTSVLCLOYDERIVTVGSSDSTVRWDNTGEVNLTLHNEAVLHLRFNSG 331
 Db 299 CKRLTGTGTSVLCLOYDERIVTVGSSDSTVRWDNTGENMLTLHNEAVLHLRFNSG 358

Qy 332 LMVTCSDKRSIAWDMASATDTLRLRVGHRAAVNVDFFDKYIVSASGDRTIKWSTS 391
 Db 359 MMVTCSDKRSIAWDMASPTDTLRLRVGHRAAVNVDFFDKYIVSASGDRTIKWNTS 418

Qy 392 TCEFVTLNGHKGIACLQYDRLVSGSSONTIRLWDIEGACLRVLEGEELVRCIRF 451
 Db 419 TCEFVTLNGHKGIACLQYDRLVSGSSONTIRLWDIEGACLRVLEGEELVRCIRF 478

Qy 452 DNKRIVSGAYDKIKWDLQALDPRAPASTCLRLVHGRVPLQDFEQIVSSHD 511
 Db 479 DNKRIVSGAYDKIKWDLQALDPRAPASTCLRLVHGRVPLQDFEQIVSSHD 538

Qy 512 DTILIWDFLNYPSSQNETRSPSRITYISR 542
 Db 539 DTILIWDFLNDAQAEPPRSPSRITYISR 569

Qy 539 DTILIWDFLNDAQAEPPRSPSRITYISR 569

RESULT 4
 US-09-601-168B-2
 Sequence 2, Application US/09601168B

GENERAL INFORMATION:
 APPLICANT: BENAROUS, Richard
 APPLICANT: MARGOTTIN, Florence
 APPLICANT: DURAND, Herve
 APPLICANT: ARENZANA SEISDEOS, Fernando
 APPLICANT: KROLL, Matthias
 APPLICANT: CONDORCET, Jean-Paul

TITLE OF INVENTION: Human beta-TrCP protein
 FILE REFERENCE: 935.38812X00
 CURRENT APPLICATION NUMBER: US/09/601,168B
 CURRENT FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: PCT/FR99/00196
 PRIOR FILING DATE: 1999-01-29
 PRIOR APPLICATION NUMBER: FR98 01100
 PRIOR FILING DATE: 1998-01-30
 PRIOR APPLICATION NUMBER: FR98 15545
 PRIOR FILING DATE: 1998-12-09
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.1 and manually
 SEQ ID NO 2
 LENGTH: 569
 TYPE: PRT
 ORGANISM: Artificial sequence
 OTHER INFORMATION: Description of the artificial sequence : cDNA
 OTHER INFORMATION: Coding for human beta-TrCP protein
 US-09-601-168B-2

Query Match Score 2384 5; DB 2; Length 569;
 Best Local Similarity 79.0%; Pred. No. 6.4e-22;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTYLMCS-----VP----RSLWGGCANLY--ESMCA 36
 Db 1 MDPAEVQLQEALKFENNSEREDCNNGEPPRKIIPEKNSLQRQTYNSCARCLNQBTVCLA 60

Qy 37 SCLQSMPSVRCL---QTSNGTSSVTYSRKPSSEGNYQEKDLCIYKFDWSESDOYEVE 93
 Db 61 S-TANKTENCYAKTKIANGTSSMIVPKQRKLSSAYKEKELCVKTFEQNSSESDQVEVE 118

Qy 94 HL1SRMCHYQHGHSINSYLKPMQLQRFDTALPEQGDHIAENILSYLDARS1CAAEVCKE 153
 Db 119 HL1SQMCHYQHGHSINSYLKPMQLQRFDTALPARGLDHIAENILSYLDAS1CAAEVCKE 178

Qy 154 WQVISEGMLWKLLIERMVRDPLWKGLSERGMDOYLKNRPTDG--PPNSFSYSLYPK 211
 Db 179 WYRVTSDGMLWKLLIERMVRDPLWKGLSERGMDOYLKNRPTDG--PPNSFSYSLYPK 238

Qy 212 IIQDIEIESNWRCRHNLRIQCESNSKGVYCLQYDDEKIKISSLDRNSIKIWKXTSLE 271
 Db 239 IIQDIEIESNWRCRHNLRIQCESNSKGVYCLQYDDEKIKISSLDRNTIKIWKNTLE 298

Qy 272 CLKVLTGTSVLCLOYDERIVTVGSSDSTVRWDNTGEVNLTLHNEAVLHLRFNSG 331
 Db 299 CKRLTGTGTSVLCLOYDERIVTVGSSDSTVRWDNTGENMLTLHNEAVLHLRFNSG 358

Qy 332 LMVTCSDKRSIAWDMASATDTLRLRVGHRAAVNVDFFDKYIVSASGDRTIKWSTS 391
 Db 359 MMVTCSDKRSIAWDMASPTDTLRLRVGHRAAVNVDFFDKYIVSASGDRTIKWNTS 418

Qy 392 TCEFVTLNGHKGIACLQYDRLVSGSSONTIRLWDIEGACLRVLEGEELVRCIRF 451
 Db 419 TCEFVTLNGHKGIACLQYDRLVSGSSONTIRLWDIEGACLRVLEGEELVRCIRF 478

Qy 452 DNKRIVSGAYDKIKWDLQALDPRAPASTCLRLVHGRVPLQDFEQIVSSHD 511
 Db 479 DNKRIVSGAYDKIKWDLQALDPRAPASTCLRLVHGRVPLQDFEQIVSSHD 538

Qy 512 DTILIWDFLNYPSSQNETRSPSRITYISR 542
 Db 539 DTILIWDFLNDAQAEPPRSPSRITYISR 569

RESULT 5
 US-08-190-802A-30
 Sequence 30, Application US/08190802A
 Patent No. 551903
 GENERAL INFORMATION:
 APPLICANT: Mochny-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: P.O. Box 60810
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306-0850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/190,802A
 FILING DATE: 01-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 8600-0139
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0860
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 517 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

US-08-190-802A-30
 Query Match Score 2286.5; DB 1; Length 517;
 Best Local Similarity 87.8%; Pred. No. 2.8e-217;

Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2; / ; TELEPHONE: (202) 887-1500
 Qy 44 SVRQLQISGTSVIVSRKPSGSNYQERDLCIJKYDQWSSDQVEREHLISRMCHYQ 103 / ; TELEFAX: (202) 887-0763
 Db 34 TLRQTKLNGTSSMIVPKQRKLSANYEKEKELCVKYFQWSBCDOFEVFEHLISRMCHYQ 93 / ; INFORMATION FOR SEQ ID NO: 30;
 Qy 104 HGHINSYLPKMLORDFTALPEOGLDHIAENILSYLDARSCLAAELYCKEWORVISSEGML 163 / ; SEQUENCE CHARACTERISTICS:
 Db 94 RGHANTYLKPMLORDFTALPEOGLDHIAENILSYLDARSCLAAELYCKEWORVISSEGML 153 / ; LENGTH: 517 amino acids
 Qy 164 WKLLIERMVRTDPWLKGSLSERGMDOYLFKNRPTDG--PNNFSYRSLYPLPKILODIEIES 221 / ; TOPology: unknown
 Db 154 WKLLIERMVRTDPWLKGSLSERGMDOYLFKNRPTDG--PNNFSYRSLYPLPKILODIEIES 213 / ; MOLECULE TYPE: peptide
 Qy 222 NWIGGRHNNQRIQCRSENSRGVTCVQYDDEKIISGLRDNLKSLCBLCKVLHTG 281 / ; HYPOThETICAL: NO
 Db 214 NWRCGRHSQTRICRSRSETSKGVYCLQYDQKIVSGLRDTNTIKWDKNTLBECKVLHTG 273 / ; ANTI-SENSE: NO
 Qy 282 SVLCLQYDERVITYGSSDSTVRYDVNTGEVNLTHHNNEAVLHRLFSNGLMVTCSKDRS 341 / ; ORIGINAL SOURCE:
 Db 274 SVLCLQYDERVITYGSSDSTVRYDVNTGEVNLTHHNNEAVLHRLFSNGLMVTCSKDRS 332 / ; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 Qy 342 IAYNDMASTDTLRRVLYGHRRAVNVDFFDKYIVSASGDRTIKVNSTSTCEFVRTLNG 401 / ; US-08-477-346-30
 Db 333 IAYNDMASTDTLRRVLYGHRRAVNVDFFDKYIVSASGDRTIKVNSTSTCEFVRTLNG 392 / ;
 Qy 402 HKRGJACIQLYDRDLUVSSGSDNTLWIEEGACLRLVGEHEELVRCKRFDNKRIVSGAY 461 / ;
 Db 393 HKRGJACIQLYDRDLUVSSGSDNTLWIEEGACLRLVGEHEELVRCKRFDNKRIVSGAY 452 / ;
 Qy 462 DGKIKWDLQALDPRAPASTLCLRTLVHSGRVFRLOPDEFQISSLHDITLIDFLN 521 / ;
 Db 453 DGKIKWDLQALDPRAPASTLCLRTLVHSGRVFRLOPDEFQISSLHDITLIDFLN 512 / ;
 Qy 522 VP 523 / ;
 Db 513 DP 514 / ;
 RESULT 6 / ;
 US-08-477-346-30 / ;
 ; Sequence 30, Application US/08477346 / ;
 ; Patent No. 6262023 / ;
 ; GENERAL INFORMATION: / ;
 ; APPLICANT: Ron, Dorit / ;
 ; APPLICANT: Mochly-Rosen, Daria / ;
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses / ;
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses / ;
 ; NUMBER OF SEQUENCES: 265 / ;
 ; CURRENT APPLICATION DATA: / ;
 ; ADDRESS: Morrison & Foerster / ;
 ; STREET: 2000 Pennsylvania Avenue, NW / ;
 ; CITY: Washington / ;
 ; STATE: DC / ;
 ; COUNTY: USA / ;
 ; ZIP: 20006-1812 / ;
 ; COUNTRY: USA / ;
 ;
 ; COMPUTER READABLE FORM: / ;
 ; MEDIUM TYPE: Floppy disk / ;
 ; COMPUTER: IBM PC compatible / ;
 ; OPERATING SYSTEM: PC DOS/MS-DOS / ;
 ; SOFTWARE: Patent Release #1.0, Version #1.2.5 / ;
 ; CURRENT APPLICATION NUMBER: US/08/477,346 / ;
 ; APPLICATION NUMBER: 08/487,072 / ;
 ; FILING DATE: 07-JUN-1995 / ;
 ; CLASSIFICATION: 514 / ;
 ; PRIORITY APPLICATION DATA: / ;
 ; APPLICATION NUMBER: 08/487,072 / ;
 ; FILING DATE: 07-JUN-1995 / ;
 ; ATTORNEY/AGENT INFORMATION: / ;
 ; NAME: MURASHIGE, KATE H. / ;
 ; REGISTRATION NUMBER: 29,959 / ;
 ; REFERENCE/DOCKET NUMBER: 2550-0025-20 / ;
 ; TELECOMMUNICATION INFORMATION: / ;
 ;

Query Match 79 4*; Score 2286.5; DB 2; Length 517; / ;
 Best Local Similarity 87.8%; Pred. No. 2.8e-217; / ;
 Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2; / ;
 Qy 44 SVRQLQISGTSVIVSRKPSGSNYQERDLCIJKYDQWSSDQVEREHLISRMCHYQ 103 / ;
 Db 34 TLRQTKLNGTSSMIVPKQRKLSANYEKEKELCVKYFQWSBCDOFEVFEHLISRMCHYQ 93 / ;
 Qy 104 HGHINSYLPKMLORDFTALPEOGLDHIAENILSYLDARSCLAAELYCKEWORVISSEGML 163 / ;
 Db 94 HGHINSYLPKMLORDFTALPEOGLDHIAENILSYLDARSCLAAELYCKEWORVISSEGML 153 / ;
 Qy 222 NWIGGRHNNQRIQCRSENSRGVTCVQYDDEKIISGLRDNLKSLCBLCKVLHTG 281 / ;
 Db 214 NWRCGRHSQTRICRSRSETSKGVYCLQYDQKIVSGLRDTNTIKWDKNTLBECKVLHTG 273 / ;
 Qy 282 SVLCLQYDERVITYGSSDSTVRYDVNTGEVNLTHHNNEAVLHRLFSNGLMVTCSKDRS 341 / ;
 Db 274 SVLCLQYDERVITYGSSDSTVRYDVNTGEVNLTHHNNEAVLHRLFSNGLMVTCSKDRS 332 / ;
 Qy 342 IAYNDMASTDTLRRVLYGHRRAVNVDFFDKYIVSASGDRTIKVNSTSTCEFVRTLNG 401 / ;
 Db 333 IAYNDMASTDTLRRVLYGHRRAVNVDFFDKYIVSASGDRTIKVNSTSTCEFVRTLNG 392 / ;
 Qy 402 HKRGJACIQLYDRDLUVSSGSDNTLWIEEGACLRLVGEHEELVRCKRFDNKRIVSGAY 461 / ;
 Db 393 HKRGJACIQLYDRDLUVSSGSDNTLWIEEGACLRLVGEHEELVRCKRFDNKRIVSGAY 452 / ;
 Qy 462 DGKIKWDLQALDPRAPASTLCLRTLVHSGRVFRLOPDEFQISSLHDITLIDFLN 521 / ;
 Db 453 DGKIKWDLQALDPRAPASTLCLRTLVHSGRVFRLOPDEFQISSLHDITLIDFLN 512 / ;
 Qy 522 VP 523 / ;
 Db 513 DP 514 / ;
 RESULT 7 / ;
 US-08-477-346-30 / ;
 ; Sequence 30, Application US/084773089 / ;
 ; Patent No. 6343368 / ;
 ; GENERAL INFORMATION: / ;
 ; APPLICANT: Mochly-Rosen, Daria / ;
 ; APPLICANT: Ron, Dorit / ;
 ; TITLE OF INVENTION: Thereof / ;
 ; NUMBER OF SEQUENCES: 265 / ;
 ; CURRENT APPLICATION DATA: / ;
 ; ADDRESS: Morrison & Foerster / ;
 ; STREET: 2000 Pennsylvania Avenue, NW / ;
 ; CITY: Washington / ;
 ; STATE: DC / ;
 ; COUNTY: USA / ;
 ; ZIP: 20006-1812 / ;
 ; COMPUTER READABLE FORM: / ;
 ;

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/473,089
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MORASHIGE, KATE H.
 REFERENCE/DOCKET NUMBER: 29, 959
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 INFORMATION FOR SEQ ID NO: 30:
 LENGTH: 517 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 US-08-473-089-30

Query Match 79.4%; Score 2266.5; DB 2; Length 517;
 Best Local Similarity 87.8%; Pred. No. 2.8e-217;
 Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2;

Qy 44 SVRCIQLNGTSSVSRKRPSEGNYQEKDLCIKYFDQWSEDQVEFVEHLISRMCHYQ 103
 Db 34 TLRQTKLANGTSSMVPKRLSANYEKEKELYKVFBNWSECQVEFVEHLISRMCHYQ 93
 Qy 104 RGHINTSYLKPMQLORDFITALPEQGLDHIAENILSYLDARSLSLCAELYCKEWORYISEGML 163
 Db 94 RGHINTSYLKPMQLORDFITALPARGLDHIAENILSYLDARSLSLCSAELYCKEWTRVTSDML 153

Qy 164 WKLLIERMVRDPLWKGLSERRGHDQYLPKQRPFDG - PPNSFYRSLMPKIQDIEITES 221
 Db 154 WKLLIERMVRDPLWRGLAERRGWQYLPKQPDGKTPNSFYRALYCKEWTRVTSDML 213

Qy 222 NWRCGRHNHQRIQCRSENSERGVYCLQYDDDEBKISLGLRDNISKIWDKTSSBCLVKLTGTG 281
 Db 214 NWRCGRHSQIQRSETSKGVNCLQYDDQKIVSLRNTIKWDKNTLECRVLMGHTG 273

Qy 282 SVLCLQYDERRVITYGSSDSTVRYDVNTGEVNTLIIHNEAVLHLRFSGNLMYTCSDRS 341
 Db 274 SVLCLQYDERRVITYG-SDSTVRYDVNTGEMNLIIHCEAVLHLRFNGMMYTCSDRS 332

Qy 342 IAVIDMASATDITURRVLYGHRAAVNVDFDDKYIVASGDRTKWNTSTCFVRTING 401
 Db 333 IAVIDMASATDITURRVLYGHRAAVNVDFDDKYIVASGDRTKWNTSTCFVRTING 392

Qy 402 HKRGIACLQYDRLVGSSESDNTTRLWDIECGACLRVLEGHEELVRCRFDNKRIVSAY 461
 Db 393 HKRGIACLQYDRLVGSSESDNTTRLWDIECGACLRVLEGHEELVRCRFDNKRIVSAY 452

Qy 462 DGKIKWMDLQAALDPRAPASTCLCLRTVYEHSGRVFRLODEFOLISSHDDTLLIWDTLN 521
 Db 453 DGKIKWMDLVAALDPRAPAGTLCLRTVYEHSGRVFRLODEFOLVSSHDDTLLIWDTLN 512

Qy 522 VP 523
 Db 513 DP 514

RESULT 8
 US-08-487-072A-30
 Sequence 1, Application US/08487072A
 i Patient No. 6423684
 ; GENERAL INFORMATION

APPLICANT: Mochly-Rosen, Daria
 APPLICANT: Ron, Dorit
 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Avenue, NW
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1812
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,072A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MORASHIGE, KATE H.
 REGISTRATION NUMBER: 29, 959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 INFORMATION FOR SEQ ID NO: 30:
 LENGTH: 517 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
 US-08-473-089-30

Query Match 79.4%; Score 2286.5; DB 2; Length 517;
 Best Local Similarity 87.8%; Pred. No. 2.8e-217;
 Matches 423; Conservative 33; Mismatches 23; Indels 3; Gaps 2;

Qy 44 SYRCLOISNGTSSVIVSRKRPSEGNYQEKDLCIKYFDQWSEDQVEFVEHLISRMCHYQ 103
 Db 34 TURQTKLANGTSSMIVPKRKLSANYEKEKELYKVFBNWSECQVEFVEHLISRMCHYQ 93
 Qy 104 HGHINTSYLKPMQLORDFITALPEQGLDHIAENILSYLDARSLSLCAELYCKEWTRVTSDML 163
 Db 94 HGHINTSYLKPMQLORDFITALPARGLDHIAENILSYLDARSLSLCSAELYCKEWTRVTSDML 153

Qy 222 NWRCGRHNQRIQCRSENSERGVYCLQYDDDEBKISLGLRDNISKIWDKTSSBCLVKLTGTG 281
 Db 214 NWRCGRHSQIQRSETSKGVNCLQYDDQKIVSLRNTIKWDKNTLECRVLMGHTG 273

Qy 282 SVLCLQYDERRVITYGSSDSTVRYDVNTGEVNTLIIHNEAVLHLRFSGNLMYTCSDRS 341
 Db 274 SVLCLQYDERRVITYG-SDSTVRYDVNTGEMNLIIHCEAVLHLRFNGMMYTCSDRS 332

Qy 342 IAVIDMASATDITURRVLYGHRAAVNVDFDDKYIVASGDRTKWNTSTCFVRTING 401
 Db 333 IAVIDMASATDITURRVLYGHRAAVNVDFDDKYIVASGDRTKWNTSTCFVRTING 392

Qy 402 HKRGIACLQYDRLVGSSESDNTTRLWDIECGACLRVLEGHEELVRCRFDNKRIVSAY 461
 Db 393 HKRGIACLQYDRLVGSSESDNTTRLWDIECGACLRVLEGHEELVRCRFDNKRIVSAY 452

Qy 462 DGKIKWMDLQAALDPRAPASTCLCLRTVYEHSGRVFRLODEFOLISSHDDTLLIWDTLN 521
 Db 453 DGKIKWMDLVAALDPRAPAGTLCLRTVYEHSGRVFRLODEFOLVSSHDDTLLIWDTLN 512

Qy 522 VP 523
 Db 513 DP 514

RESULT 8
 US-08-487-072A-30
 Sequence 1, Application US/08487072A
 i Patient No. 6423684
 ; GENERAL INFORMATION

APPLICANT: Li, Jinhe
 APPLICANT: Pauley, Adele M.
 APPLICANT: Pharmacia & Upjohn Company
 TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 FILE REFERENCE: 6142
 CURRENT APPLICATION NUMBER: US/09/213, 888A
 NUMBER OF SEQ ID NOS: 27
 CURRENT FILING DATE: 1998-12-17
 SEQ ID NO: 7
 LENGTH: 540
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-213-888-7

Query Match 22.3%; Score 641.5; DB 2; Length 540;
 Best Local Similarity 32.1%; Pred. No. 2.1e-54;
 Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;

Qy 77 IKYFDQNSESDQVEFVHLISRMCYQHGHINSYKPMQLQRDETTALPEQGLDHIAENIL 136
 Db 71 LKMFQSGPKEKLALDELIDSCPTQVKHMMQVIEPQFRDSLPE--LALYVL 126

Qy 137 SYLDARSUCAELVCKEWRQVISSEGMLWKKLIERMVRTDPWKLSERRGWDQYL-FKNR 195
 Db 127 SFLPKDLIQAQTCRYW-RILAEDNL-----LVRKCCKEIGIDEPLHTKRR 172

Qy 196 PTDCPPNSFYRSLYPKIQDIEETESNWRCGRNHLQR1QCRSENSKGYVCLQYDDEKLIS 255
 Db 173 KVKP--GFIHSPPWSAVRQHRDTNWRRGELKSPKV-LKGHDHVTCLQFCGNRIVS 229

Db 256 GLRDNSIKIWWDKTSLECLKVLTGHGTGSVLCQYDERYVITVGSSDSTVRWDVNTGEVLNT 315
 Db 230 GSDNTLKVWSAVGKCLRTLVHTGGWSSONQRDNIIISGSTRTKWNAAEGCITH 289

Qy 316 LIHNEAVLHLRFPSGLMNTCSKDRSATIWLRRVLUFGHRAAVNVDFDDKY 375
 Db 290 LYGHSTSIVRCMHILKRVVSGSRDATLRVWDTETGQCL--HYLMGHVAAYRCVQYDGR 346

Db 376 IVSASGDRTIKWSTSTCEVRTLNGHKGRIACLYQDRRLVYSSDNTIRLWDIECGAC 435
 Db 347 VWSGAYDPMKWVDPETCTCLHFLQGHTNRYSLQFDGIHVSGSLOTSIRWDVETGNC 406

Qy 436 LRVLEGHEELVRVCIRFDNKRIVSGAYDGKWKDQLQALDPRAPASTICLRTLIV--EHS 492
 Db 407 IHTLGHQSLTSMEKDNLVYSGNADESTVKTWIKRG-----OCLQTLOGPNHQ 457

Qy 493 GRVPRLOPDEFQLISSSHDDTLLIWD 518
 Db 458 SAVTCLOFMKNFVYTSSDGTVKLWD 483

RESULT 13
 US-09-328-877D-7
 Sequence 7, Application US/09328877D
 Patent No. 6730778
 GENERAL INFORMATION:
 APPLICANT: Li, Jinhe
 APPLICANT: Pauley, Adele M.
 APPLICANT: Pharmacia & Upjohn Company
 TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 TITLE OF INVENTION: Encode Them
 FILE REFERENCE: 6142
 CURRENT APPLICATION NUMBER: US/09/328, 877D
 CURRENT FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 32
 SEQ ID NO 7
 LENGTH: 540
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-328-877D-7

Query Match 22.3%; Score 641.5; DB 2; Length 540;
 Best Local Similarity 32.1%; Pred. No. 2.1e-54;
 Matches 143; Conservative 89; Mismatches 177; Indels 37; Gaps 9;

Qy 77 IKYFDQNSESDQVEFVHLISRMCYQHGHINSYKPMQLQRDETTALPEQGLDHIAENIL 136
 Db 71 LKMFQSGPKEKLALDELIDSCPTQVKHMMQVIEPQFRDSLPE--LALYVL 126

Qy 137 SYLDARSUCAELVCKEWRQVISSEGMLWKKLIERMVRTDPWKLSERRGWDQYL-FKNR 195
 Db 127 SFLPKDLIQAQTCRYW-RILAEDNL-----LVRKCCKEIGIDEPLHTKRR 172

196 PTDGPNSFYRSLYPKIQQDIEIESNWRGRHNLQRIQRSENSKGVYCLQYDDBKITS 255
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 173 KV1KP--GFIHPWKSAYIQRHRIDTNRREBLKSPKV-LKGHDHVVITCQFCNRIVS 229
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 256 GLRDNSIKIWDTKSLEBLKVLTGHTSVLCLQYDERVITVCGSSDSTVRYWDVNTEGVLT 315
 Db 230 GSDNTLKWASAVTKCRLTVLGHTGGWSQMRDNITISSTDRTLKVNAAETGECHT 289
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 316 LIHNEAVLHLRFNSNGIMVTCSDKRSTAVMADATDITLRLRVYDFFDKY 375
 Db 290 LYGHSTVRCMHLHEGRVSGSRDATLRLWDETGCL--HVLMGHVAARCVYDGR 346
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 346 IYSGASGRTIKWSTSTCEFRTLNGHKGIAQYDRLVYVSGSSDNTIRLWDLIECGAC 435
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 347 VVSGAYDFMVKWDMPETEBCUFLQHTQHTRNRYSLQPDGIHVSGSDBTSIRWVDVETGNC 406
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 436 LRVLEGHEELVRCIRFDNKRVISGAYDGKIKWDLQALDPRAPASTLCLRTLV--EHS 492
 Db 407 IHTLTGHQSLSITSGMELKDNILVSGNADSTVKICWDLIKTG-----QCLQZQPNKHQ 457
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 493 GRVERLQDFEQIISSSHDDTILWD 518
 Db 458 SAVTCLQFNKFVITSSDDGTVKLWD 483
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 458 SAVTCLQFNKFVITSSDDGTVKLWD 483

RESULT 15
 US-09-213-888-6
 ; Sequence 6, Application US/09213888A
 ; Patent No. 6638711
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.
 ; INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 ; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 ; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
 ; APPLICANT: Pharmacia & Upjohn Company
 ; FILE REFERENCE: 6142
 ; CURRENT APPLICATION NUMBER: US/09/213,888A
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 545
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-213-888-6

Query Match 22.3%; Score 641.5; DB 2; Length 545;
 Best Local Similarity 32.1%; Pred. No. 2.1e-54;
 Matches 143; Conservative 89; Mismatches 37; Gaps 9;

Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 76 LRMFQSWSGPBKLLAEDLDSCTPTQVKHMMOVIEPQFQDFISLPLKE--LALYVL 131
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 137 SYLDARSILCAELVCKEWQRVISSEGMLWKLLIERMVRDPLWKGLSERRGWDQYL-FKNR 195
 Db 132 SFLEPKDQLQQAQTCRYW-RILAEDNL-----LWRECKKEBGEDEPHIKR 177
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 196 PTDGPNSFYRSLYPKIQQDIEIESNWRGRHNLQRIQRSENSKGVYCLQYDEKKIS 255
 Db 178 KV1KP--GFIHPWKSAYIQRHRIDTNRREBLKSPKV-LKGHDHVVITCQFCNRIVS 234
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 256 GLRDNSIKIWDTKSLECLQVCLTGHGSVLCQYDDEVITVCGSSDSTVRYWDVNTEGVLT 315
 Db 235 GSDNTLKWASAVTKCRLTVLGHTGGWSQMRDNITISSTDRTLKVNAAETGECHT 294
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 316 LIHNEAVLHLRFNSNGIMVTCSDKRSTAVMADATDITLRLRVYDFFDKY 375
 Db 329 LYGHSTVRCMHLHEGRVSGSRDATLRLWDETGCL--HVLMGHVAARCVYDGR 351
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 376 IVSASDRTIKWSTSTCEVRTLGHKGIAQYDRLVYVSGSSDNTIRLWDEBCGAC 435
 Db 352 VVSGAYDEMVKWDPETETCLHTLQHTQHTRNRYSLQPDGIHVSGSDBTSIRWVDVETGNC 411
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 127 SFLEPKDQLQQAQTCRYW-RILAEDNL-----LWRECKKEBGEDEPHIKR 172
 Db 128 GLRDNSIKIWDTKSLECLQVCLTGHGSVLCQYDDEVITVCGSSDSTVRYWDVNTEGVLT 315
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 196 PTDGPNSFYRSLYPKIQQDIEIESNWRGRHNLQRIQRSENSKGVYCLQYDDEKKIS 255
 Db 173 KV1KP--GFIHPWKSAYIQRHRIDTNRREBLKSPKV-LKGHDHVVITCQFCNRIVS 229
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 256 GLRDNSIKIWDTKSLECLQVCLTGHGSVLCQYDDEVITVCGSSDNTIRLWDEBCGAC 435
 Db 230 GSDNTLKWASAVTKCRLTVLGHTGGWSQMRDNITISSTDRTLKVNAAETGECHT 289
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 316 LIHNEAVLHLRFNSNGIMVTCSDKRSTAVMADATDITLRLRVYDFFDKY 375
 Db 329 LYGHSTVRCMHLHEGRVSGSRDATLRLWDETGCL--HVLMGHVAARCVYDGR 346
 Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 376 IVSASDRTIKWSTSTCEVRTLGHKGIAQYDRLVYVSGSSDNTIRLWDEBCGAC 435

Search completed: August 25, 2006, 07:24:10
 Job time : 51 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 25, 2006, 07:34:43 ; Search time 185 Seconds
(without alignments)

Title: US-10-665-715-16
Perfect score: 2879
Sequence: 1 MEPDSVIEDKTELMCSVPR.....DPSAQNETRSPSRYYISR 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 209797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us10_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/us11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	3 US-09-832-161-16	Sequence 16, Appl
2	2879	100.0	542	4 US-09-832-161-16	Sequence 16, Appl
3	2384.5	82.8	569	3 US-09-832-161-18	Sequence 18, Appl
4	2384.5	82.8	569	4 US-10-042-417-2	Sequence 2, Appl
5	2384.5	82.8	569	4 US-10-038-010-8	Sequence 8, Appl
6	2384.5	82.8	569	4 US-10-665-715-18	Sequence 18, Appl
7	2384.5	82.8	569	5 US-10-652-928-2	Sequence 2, Appl
8	2384.5	82.8	569	5 US-10-632-150-2	Sequence 2, Appl
9	2384.5	82.8	569	6 US-11-073-485-2	Sequence 2, Appl
10	2384.5	82.8	569	6 US-11-073-470-2	Sequence 2, Appl
11	2384.5	82.8	569	6 US-11-073-457-2	Sequence 2, Appl
12	2384.5	82.8	569	6 US-11-099-691-12	Sequence 12, Appl
13	2384.5	82.8	569	6 US-11-073-460-2	Sequence 2, Appl
14	2375.5	82.5	569	4 US-10-687-732-18	Sequence 18, Appl
15	2077.5	72.2	510	6 US-11-097-143-6363	Sequence 6363, Appl
16	2002	69.5	408	4 US-10-687-732-15	Sequence 15, Appl
17	1829.5	63.5	407	4 US-10-687-732-14	Sequence 14, Appl
18	1638.5	56.9	701	4 US-10-369-493-5420	Sequence 5420, Appl
19	1525.5	53.0	424	4 US-10-687-732-13	Sequence 13, Appl
20	1143	39.7	265	3 US-09-764-848-30	Sequence 30, Appl
21	1143	39.7	265	4 US-10-116-016-30	Sequence 30, Appl
22	1143	39.7	265	4 US-10-222-020-30	Sequence 30, Appl
23	693.5	24.1	219	4 US-10-023-330-2	Sequence 2, Appl
24	654	22.7	1326	6 US-11-097-143-28503	Sequence 28503, Appl
25	654	22.7	1326	6 US-11-097-143-28506	Sequence 28506, Appl
26	654	22.7	1326	6 US-11-097-143-36945	Sequence 36945, Appl
27	643	22.3	626	3 US-09-213-888-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-832-161-16
; Sequence 16, Application US/09832161.
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yonon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF NF-
; TITLE OF INVENTION: NF-kB
; FILE REFERENCE: 860098-427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIORITY APPLICATION NUMBER: 1998-12-10, 060
; PRIORITY FILING DATE: 1998-12-10
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-16

Query Match 100.0%; Score 2879; DB 3; Length 542;
Best local Similarity 100.0%; Pred. No. 1..3-e-244;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPPSVIENDKTIELMCSPYRSLMIGCANLIVESNCALSCQSMPSVRCLQISNGTSSVIVS 60
Db 1 MEPPSVIENDKTIELMCSPYRSLWIGCANLIVESNCALSCQSMPSVRCLQISNGTSSVIVS 60

Qy 61 RKRSEGNYQKEKDLCIKYFDQNSESDQEVBFHLLSMCHYQGHINSYLKPKMLQRDFI 120
Db 61 RKRSEGNYQKEKDLCIKYFDQNSESDQEVBFHLLSMCHYQGHINSYLKPKMLQRDFI 120

Qy 121 TALPEQGLDHIAENILSYLDARSICAAELVCKEWQRVISGMLWKKLIERMVTDPWKKG 180
Db 121 TALPEQGLDHIAENILSYLDARSICAAELVCKEWQRVISGMLWKKLIERMVTDPWKKG 180

Qy 181 LSERGRGWDOLFKRNPPTGPPNSYRSLYPKIQDIETESNRGRHNLRQCRSENS 240
Db 181 LSERGRGWDOLFKRNPPTGPPNSYRSLYPKIQDIETESNRGRHNLRQCRSENS 240

Qy 241 KGTYCLOYDDEKITSGLRDNSIKWDTSLECLRVLTKHTGVSYCLQYDERVTVGSSD 300
Db 241 KGTYCLOYDDEKITSGLRDNSIKWDTSLECLRVLTKHTGVSYCLQYDERVTVGSSD 300

Db	241 KGVYCLQYDDEKISGLRDNSIKIWDTKSLECLKVLTGHTGSVLQYDERRIVTGSSDS 300	Db	241 KGVYCLQYDDEKISGLRDNSIKIWDTKSLECLKVLTGHTGSVLQYDERRIVTGSSDS 300
Qy	301 TWRWDNTGEVINTLHHNEAVLHRSFNGMVTCSKDRIIAVWMSAATDITURRLV 360	Qy	301 TWRWDNTGEVINTLHHNEAVLHRSFNGMVTCSKDRIIAVWMSAATDITURRLV 360
Db	301 TWRWDNTGEVINTLHHNEAVLHRSFNGMVTCSKDRIIAVWMSAATDITURRLV 360	Db	301 TWRWDNTGEVINTLHHNEAVLHRSFNGMVTCSKDRIIAVWMSAATDITURRLV 360
Qy	361 GHRRAVNVDFFDKYIVASGDRTIKWSTSTCEFTVLNKHKGTAICLQYDRDLVSGS 420	Qy	361 GHRRAVNVDFFDKYIVASGDRTIKWSTSTCEFTVLNKHKGTAICLQYDRDLVSGS 420
Db	361 GHRRAVNVDFFDKYIVASGDRTIKWSTSTCEFTVLNKHKGTAICLQYDRDLVSGS 420	Db	361 GHRRAVNVDFFDKYIVASGDRTIKWSTSTCEFTVLNKHKGTAICLQYDRDLVSGS 420
Qy	421 SDNTIRLWDEGACLRVLEGEELVRCDPDKRIVSGAYDGKIKWDLQAAQDPRAPA 480	Qy	421 SDNTIRLWDEGACLRVLEGEELVRCDPDKRIVSGAYDGKIKWDLQAAQDPRAPA 480
Db	421 SDNTIRLWDEGACLRVLEGEELVRCDPDKRIVSGAYDGKIKWDLQAAQDPRAPA 480	Db	421 SDNTIRLWDEGACLRVLEGEELVRCDPDKRIVSGAYDGKIKWDLQAAQDPRAPA 480
Qy	481 STLCRLTVEHSGRVFRILQFDQIISSHDDTILWDFLNVPSSAQNETRSPRTYTYI 540	Qy	481 STLCRLTVEHSGRVFRILQFDQIISSHDDTILWDFLNVPSSAQNETRSPRTYTYI 540
Db	481 STLCRLTVEHSGRVFRILQFDQIISSHDDTILWDFLNVPSSAQNETRSPRTYTYI 540	Db	481 STLCRLTVEHSGRVFRILQFDQIISSHDDTILWDFLNVPSSAQNETRSPRTYTYI 540
Qy	541 SR 542	Qy	541 SR 542
Db	541 SR 542	Db	541 SR 542
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RESULT 3			
US-09-832-161-18			
; Sequence 18, Application US/10665715			
; Publication No. US20040203098A1			
; GENERAL INFORMATION			
; APPLICANT: Manning, Anthony M.			
; APPLICANT: Mercurio, Frank			
; APPLICANT: Amit, Sharon			
; APPLICANT: Ben-Neriah, Yinon			
; APPLICANT: Davis, Matti			
; APPLICANT: Hatzubai, Ada			
; APPLICANT: Lavon, Iris			
; APPLICANT: Yaron, Avraham			
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF			
; TITLE OF INVENTION: NF-KB			
; FILE REFERENCE: 860098.427			
; CURRENT APPLICATION NUMBER: US/09/832,161			
; CURRENT FILING DATE: 2001-04-09			
; PRIORITY NUMBER: 09/210,060			
; PRIORITY FILING DATE: 1998-12-10			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 16			
; LENGTH: 542			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-665-715-16			
Query Match 100.0% Score 2879; DB 4; Length 542;			
Best Local Similarity 100.0% Pred. No. 1.3e-244; Mismatches 0; Indels 0; Gaps 0;			
Matches 542; Conservative 0; Mismatches 0; Indels 31; Gaps 7;			
Qy 1 MEPSVIDEKTIELMCMSVPRSLWIGCANLVEVSNCALCLOSMPSVRCIQLISNGTSSVVS 60			
Dy 1 MEPSVIDEKTIELMCMSVPRSLWIGCANLVEVSNCALCLOSMPSVRCIQLISNGTSSVVS 60			
Qy 61 RKRESEGNYQEKDLCIKYFDONSESDQVEFVHLISMCHYQHGHINSYLPMLQDFI 120			
Dy 61 RKRESEGNYQEKDLCIKYFDONSESDQVEFVHLISMCHYQHGHINSYLPMLQDFI 120			
Qy 121 TALPEQGLHIAENTLSYLDARSICLAEVKEWQRVSEGMLWKKLTERMYRTDPLWKG 180			
Dy 121 TALPEQGLHIAENTLSYLDARSICLAEVKEWQRVSEGMLWKKLTERMYRTDPLWKG 180			
Qy 181 LSERRGMDOYLXFKNRPTDGPNSFYRSLYPKIODOIEETSWRGRHINLQRIQCRSENS 240			
Dy 181 LSERRGMDOYLXFKNRPTDGPNSFYRSLYPKIODOIEETSWRGRHINLQRIQCRSENS 240			
Qy 241 KGVYCLQYDDEKISGLRDNSIKIWDTKSLECLKVLTGHTGSVLCLOYDERIVTGSSDS 300			
Dy 241 KGVYCLQYDDEKISGLRDNSIKIWDTKSLECLKVLTGHTGSVLCLOYDERIVTGSSDS 300			
Query Match 82.8% Score 2384.5; DB 3; Length 569;			
Best Local Similarity 79.0% Pred. No. 5.3e-201; Matches 451; Conservative 48; Mismatches 45; Indels 31; Gaps 7;			
Qy 1 NEP-DSYVDEKTIELMCMSVPRSLWIGCANLVEVSNCALCLOSMPSVRCIQLISNGTSSVVS 60			
Dy 1 NEPDAEVLQERALKFNNISSEREDCNGEPPRKIIPEKNSLQTYNSCARLCLNQETVCLA 60			
Qy 37 SCLQSMPSVRCIQLISNGTSSVVS 93			
Dy 61 S-TAMKTEVCVAKTULANGTSMMIVPQRKLSASTEKEKELCVKYPEQWSSESQDVFVE 118			
Qy 94 HLISRMCHYOHGHINSYLPMLQDFI TALPEQGLHIAENTLSYLDARSICLAEVKEWQRVSEGMLWKKLTERMYRTDPLWKG 153			
Dy 119 HLISRMCHYOHGHINSYLPMLQDFI TALPEQGLHIAENTLSYLDARSICLAEVKEWQRVSEGMLWKKLTERMYRTDPLWKG 178			
Qy 154 WORVISEBMLWKKLTERMYRTDPLWKKLTERMYRTDPLWKG 211			
Dy 179 WTRVTSGMLWKKLTERMYRTDPLWKG 238			
Qy 212 IIGDIEIESWRGRHINLQRIQCRSENSKGYCLQYDDEKISGLRDNSIKIWDTKSLE 271			

b	b	239	I IQDIEIESWRGRHNSLQRHCRSETSKGVYCLQYDDQKIVSGIRDNTIKIWDTNLE	298
b	b	272	CLKVLGHTGSVLCLOYDERVITYGSSDSTYRVWDYNTGEVINTLJTHNEAVLHLRFNSG	331
b	b	299	CKRILGHTGSVLCLOYDERVITYGSSDSTYRVWDYNTGENMLNTLJTHCEAVLHLRFNNG	358
b	b	332	LMVTSKDRSTAVIDWMSATDITLRLVLUGRRAANVVDFDDKYIVSASGRTIKWNTS	391
b	b	359	MMVTSKDRSTAVIDWMSAPTDITLRLVLUGRRAANVVDFDDKYIVSASGRTIKWNTS	418
b	b	392	TCEFVTLNGHGRGIAQLQYDRLVYGSNSDTIRLWIDIEGACRVLGEHEELRCIRF	451
b	b	419	TCEFVTLNGHGRGIAQLQYDRLVYGSNSDTIRLWIDIEGACRVLGEHEELRCIRF	478
b	b	452	DNKRVTSAYDGKIKWDLQALDPRAPASTICLRTLVEHSGRVFLQDEFQIYSSSHD	511
b	b	479	DNKRVTSAYDGKIKWDLVAALDPRAPGTICLRTLVEHSGRVFLQDEFQIYSSSHD	538
b	b	512	DTILWDFLNYPSSAQNETRSPRSRTYISR	542
b	b	539	DTILWDFLNDAQAEPPRSRTYISR	569
RESULT 4				
S-10-042-417-2				
Sequence 2, Application US/10042417				
Publication No. US20020123082A1				
GENERAL INFORMATION:				
APPLICANT: Pagano, M.				
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF				
TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS				
FILE REFERENCE: 5914-090-999				
CURRENT APPLICATION NUMBER: US/10/042,417				
CURRENT FILING DATE: 2002-01-07				
PRIOR APPLICATION NUMBER: 60/260,179				
NUMBER OF SEQ ID NOS: 89				
SOFTWARE: Patentin Ver. 2.0				
SEQ ID NO 2				
LENGTH: 569				
TYPE: PRT				
ORGANISM: Homo sapiens				
S-10-042-417-2				
Query Match Score 2384 5; DB 4; Length 569;				
Best Local Similarity 79.0%; Pred. No. 5.3e-201; Mismatches 41; Indels 31; Gaps 7;				
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;				
1 MEP-DSYIEDKTIELMCS-----VP-----RSLWIGCANLY--ESMCAL 36				
1 MDPAEAVLQEALKFNNNSEREDCNGEPPRKIIPEKNSLQRQTYNSCARLCLNQEVCLAA 60				
37 SCLQSNPSPVRCL---QISNGTSTVVSRKPSSEGNYQKEKDLCIXYFDQNSBDOVEFVE 93				
61 S---TANKTENCVAKTKLNGTSSMIIPQKRKLSSAEEKERLKVYFEQNSESDQEFEVFE 118				
94 HLISOMCHYQHGHINSYLKPMQLQRFDTALPEOGDHLAENILSYLDARSLSIKAELVCKE 153				
119 HLISOMCHYQHGHINSYLKPMQLQRFDTALPARGDHLAENILSYLDAKSLCAELVCKE 178				
154 WQVISGMLWKKLIERMVRDPLWGLSERGWQYLFKNRPTDG - PNSFSYRLYPK 211				
179 WYRTSDGMWKKLIERMVRDLSLWGLAERRGWQYLFKNKPKPDPGNAPPNSFYRALYPK 238				
212 I IQDIEIESWRGRHNLQRQCRSEN SKGVYCLQYDKEK11 SIGARDNSXIKWDTNLE				
239 I IQDIEIESWRGRHNLQRHCRSETSKGVYCLQYDDQKIVSGIRDNTIKIWDTNLE				
272 CLKVLGHTGSVLCLOYDERVITYGSSDSTYRVWDYNTGEVINTLJTHNEAVLHLRFNSG				
299 CKRILGHTGSVLCLOYDERVITYGSSDSTYRVWDYNTGENMLNTLJTHCEAVLHLRFNNG				
332 LMVTSKDRSTAVIDWMSATDITLRLVLUGRRAANVVDFDDKYIVSASGRTIKWNTS				

Db	359	MWYTCOKRSIAWMDMASPDITLRLVYGHRAANVVDFDDKYIVSAGDRTIKWNTS	418
Qy	392	TCEVRTLNGHKGACIQLQYKWDLOAALDRAPASTLCLRTLVEHSGRVFLQDFEQIISSSH	451
Db	419	TCEVRTLNGHKGACIQLQYKWDLOAALDRAPASTLCLRTLVEHSGRVFLQDFEQIISSSH	478
Qy	452	DNRKIVSGAYDGKIKWDLQOALDRAPASTLCLRTLVEHSGRVFLQDFEQIISSSH	511
Db	479	DNRKIVSGAYDGKIKWDLQOALDRAPASTLCLRTLVEHSGRVFLQDFEQIISSSH	538
Qy	512	DTLILWDFLNVPSSAQNETRSPSRITYYSR	542
Db	539	DTLILWDFLNPAQAEPPRSPSRITYYSR	569
RESULT 5			
	US-10-038-010-8		
;	Sequence 8, Application US/10038010		
;	Publication No. US20030040089A1		
;	GENERAL INFORMATION:		
;	APPLICANT: HYBRIDGENICS		
;	APPLICANT: Pierre, Leigrain		
;	TITLE OF INVENTION: Peptain-protein interactions in adipocyte cells		
;	FILE REFERENCE: B477A		
;	CURRENT APPLICATION NUMBER: US/10/038, 010		
;	CURRENT FILING DATE: 2004-07-23		
;	PRIOR APPLICATION NUMBER: US 60/259, 377		
;	PRIOR FILING DATE: 2001-01-02		
;	NUMBER OF SEQ ID NOS: 67		
;	SOFTWARE: Patentin version 3.1		
;	SEQ ID NO 8		
;	LENGTH: 569		
;	TYPE: PRT		
;	ORGANISM: Homo sapiens		
;	FEATURE:		
;	NAME/KEY: beta-TRCP1		
;	LOCATION: (1)..(569)		
;	OTHER INFORMATION:		
	US-10-038-010-8		
Query Match			
	Best Local Similarity 79.0% ; Pred. No. 5.3e-201; Mismatches 48; Indels 41; Gaps 31;		
	Matches 451; Conservative 48; Score 2384.5; DB 4; Length 569;		
Qy	1	MEP-DSVTEDKTIBLMCS-----VP-----RSLWLIGCANLV--ESMCAL 36	
Db	1	MDPAEAVLQKALKMNSSPREDCNNGEPPRKIIPERNSLRQTYNCSARLCLNQETVCLA 60	
Qy	37	SCLOSSMPSYRCL---QISNGTSSVYVSRSKRPSGEHYQKEKDLCIKYPDWSESDQVEFVE	93
Db	61	S---TAMKTCNCVAKTKLANTCCTSMVPKORKLASSYEKEKELCVKYZFEQWSESDQVEFVE	118
Qy	94	HLISRMCHYQGHGHTNSYLKEMPLQRDFITALPEQGQDHIAENLSTYDARSCLAAELYCKB	153
Db	119	HLSIQSMCHYQGHGHTNSYLKEMPLQRDFITALPARGDHIAENLSTYDARSCLAAELYCKB	178
Qy	154	WORYTSEGMLWKLLIERTMYRTDPLWKGLSERRGNDYQFLKNRPTDG--PPNISFYRSLYPK	211
Db	179	WYRFTGMLWKLLIERTMYRTDLSRGLAERRGCGYQFLKNPKPDGNAPPNSFYRALYPK	238
Qy	212	IQQDIEETISNWRCGRHNLRQIOQCRSENSKGVYCYQYDDEKEIISGLRDNSTSKIKWDTKSLE	271
Db	239	IQQDIEETISNWRCGRHSLSQRIHCSETSKGVYCYQYDQDKIVSGIRDNTTSKIKWDTKITLE	298
Qy	272	CLKVLTGHTGSVLCIQLQYDERIVITGSSDSTYRWDUNTEVINTLTHHNEAVHLRFNSG	331
Db			
Qy	332	LMTYTCOKRSIAWMDMASATDITLRLVYGHRAANVVDFDDKYIVSAGDRTIKWNTS	391
Db	359	MWYTCOKRSIAWMDMASPDITLRLVYGHRAANVVDFDDKYIVSAGDRTIKWNTS	418
Qy	390	KRITLGHTRGSVLCIQLQYDERIVITGSSDSTYRWDUNTEVINTLTHHNEAVHLRFNSG	358

Qy	392 TCEFYRTLNGHKRGIACLQYDRLLVYSSDNTIRLWDEGACIIRVLGEHEELVRCIRF 451	Qy	392 TCEFYRTLNGHKRGIACLQYDRLLVYSSDNTIRLWDEGACIIRVLGEHEELVRCIRF 451
Db	419 TCEFYRTLNGHKRGIACLQYDRLLVYSSDNTIRLWDEGACIIRVLGEHEELVRCIRF 478	Db	419 TCEFYRTLNGHKRGIACLQYDRLLVYSSDNTIRLWDEGACIIRVLGEHEELVRCIRF 478
Qy	452 DNKRIVSGAYDGKIKWDLQALDPAPASTICLRLTVEHSGRVERLQDFEQLISSHD 511	Qy	452 DNKRIVSGAYDGKIKWDLQALDPAPASTICLRLTVEHSGRVERLQDFEQLISSHD 511
Db	479 DNKRIVSGAYDGKIKWDLQALDPAPASTICLRLTVEHSGRVERLQDFEQLISSHD 538	Db	479 DNKRIVSGAYDGKIKWDLQALDPAPASTICLRLTVEHSGRVERLQDFEQLISSHD 538
Qy	512 DTILWDFNVPSPQAQNTRSPSRTYISR 542	Qy	512 DTILWDFNVPSPQAQNTRSPSRTYISR 542
Db	539 DTILWDFNLPDAQAEPSPRSRTYISR 569	Db	539 DTILWDFNLPDAQAEPSPRSRTYISR 569
RESULT 6			
US-10-665-715-18			
; Sequence 18, Application US/10665715			
; Publication No. US20040203098A1			
; GENERAL INFORMATION:			
; APPLICANT: Manning, Anthony M.			
; APPLICANT: Mercurio, Frank			
; APPLICANT: Amit, Sharon			
; APPLICANT: Davis, Matti			
; APPLICANT: Hatzubai, Ada			
; APPLICANT: Lavon, Iris			
; APPLICANT: Yaron, Avraham			
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF			
; TITLE OF INVENTION: NF-KB			
; FILE REFERENCE: 860098-427			
; CURRENT APPLICATION NUMBER: US/10/665-715			
; CURRENT FILING DATE: 2003-09-19			
; PRIORITY APPLICATION NUMBER: US/09/210,060			
; PRIORITY FILING DATE: 1998-12-10			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 18			
; LENGTH: 569			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-665-715-18			
Query Match 82.8%; Score 2384.5; DB 4; Length 569;			
Best Local Similarity 79.0%; Pred. No. 5.3e-201; Mismatches 48; Indels 31; Gaps 7;			
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;			
Query 1 NEP-DSYIEDKTIELMCS-----VP----RSLWLGCAVN--ESMCAL 36			
Db 1 MDPAEAVLQEALKFMNSSEREDCNNGEPPRKIIPEKNNSROTYNSCARLCLNOETVLA 60			
Query 37 SCLQSMPSVRCL---QISNGTSSVIVSRKRSEGYNYOKEDOLCIKYFDQNSESDOVFVE 93			
Db 61 S---TAMKTCENCVAKTLANGTSMIVPKRKSASSTEREKIECVKFFQWSQSDQBFVE 118			
Query 94 HLISRMCHYQGHGINSYKLPMQLQDFITALPBOGLDHIAENILSYLDARSILCAAELVCKE 153			
Db 119 HLISQMCHYQGHGINSYKLPMQLQDFITALPARGLDHIAENILSYLDASKLCAAELVCKE 178			
Query 154 WORVISEGMWLWKLLIERNVRTPLWKGLISERGWQDYLQRPRPTDG--PPNSFYRSLYPK 211			
Db 179 WYRVTSQDMWLWKLLIERNVRTDSLWKGIAERGWQDYLQRPRPTDG--PPNSFYRSLYPK 238			
Query 212 IQDIETIESNWRCGRHNLRQIOCRSENSKGYYCLOYDKEKISGLRDNSIKIWDKTSL 271			
Db 239 IQDIETIESNWRCGRHNLRQIOCRSENSKGYYCLOYDKEKISGLRDNSIKIWDKTSL 298			
Query 272 CLKVLTGHTGSVLCLOYDKEVNTGSSSTYRVWDNTGEVNTLTHNEAVLHLRFNSG 331			
Db 299 CKRILTGTGHTGSVLCLOYDKEVNTGSSSTYRVWDNTGEVNTLTHNEAVLHLRFNSG 358			
Query 332 LMVTCSDRSIAVWDMASATDTLRRVLYGHRRAAVNVDFDDKYIVSASGDRTIKWSTS 391			
Db 359 LMVTCSDRSIAVWDMASPTDTLRRVLYGHRRAAVNVDFDDKYIVSASGDRTIKWSTS 418			
RESULT 7			
US-10-652-928-2			
; Sequence 2, Application US/10652928			
; Publication No. US20050079558A1			
; GENERAL INFORMATION:			
; APPLICANT: Chiaur, D.			
; APPLICANT: Pagano, M.			
; APPLICANT: Latres, E.			
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS			
; CURRENT APPLICATION NUMBER: US/10/652, 928			
; CURRENT FILING DATE: 2003-08-28			
; PRIOR APPLICATION NUMBER: 5914-081			
; FILE REFERENCE: 5914-081			
; PRIOR FILING DATE: 1999-08-27			
; PRIOR APPLICATION NUMBER: 60/098, 355			
; PRIOR FILING DATE: 1998-08-28			
; PRIOR APPLICATION NUMBER: 60/118, 568			
; PRIOR FILING DATE: 1999-02-03			
; PRIOR APPLICATION NUMBER: 60/124, 449			
; PRIOR FILING DATE: 1999-03-15			
; NUMBER OF SEQ ID NOS: 90			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 569			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-652-928-2			
Query Match 82.8%; Score 2384.5; DB 5; Length 569;			
Best Local Similarity 79.0%; Pred. No. 5.3e-201; Mismatches 48; Indels 31; Gaps 7;			
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;			
Query 1 MEP-DSYIEDKTIELMCS-----VP----ESMCAL 36			
Db 1 MDPAEAVLQEALKFMNSSEREDCNNGEPPRKIIPEKNNSROTYNSCARLCLNOETVLA 60			
Query 37 SCLQSMPSVRCL---QISNGTSSVIVSRKRSEGYNYOKEDOLCIKYFDQNSESDOVFVE 93			
Db 61 S---TAMKTCENCVAKTLANGTSMIVPKRKSASSTEREKIECVKFFQWSQSDQBFVE 118			
Query 94 HLISRMCHYQGHGINSYKLPMQLQDFITALPBOGLDHIAENILSYLDARSILCAAELVCKE 153			
Db 119 HLISQMCHYQGHGINSYKLPMQLQDFITALPARGLDHIAENILSYLDASKLCAAELVCKE 178			
Query 154 WORVISEGMWLWKLLIERNVRTPLWKGLISERGWQDYLQRPRPTDG--PPNSFYRSLYPK 211			
Db 179 WYRVTSQDMWLWKLLIERNVRTDSLWKGIAERGWQDYLQRPRPTDG--PPNSFYRSLYPK 238			
Query 212 IQDIETIESNWRCGRHNLRQIOCRSENSKGYYCLOYDKEKISGLRDNSIKIWDKTSL 271			
Db 239 IQDIETIESNWRCGRHNLRQIOCRSENSKGYYCLOYDKEKISGLRDNSIKIWDKTSL 298			
Query 272 CLKVLTGHTGSVLCLOYDKEVNTGSSSTYRVWDNTGEVNTLTHNEAVLHLRFNSG 331			
Db 299 CKRILTGTGHTGSVLCLOYDKEVNTGSSSTYRVWDNTGEVNTLTHNEAVLHLRFNSG 358			
Query 332 LMVTCSDRSIAVWDMASATDTLRRVLYGHRRAAVNVDFDDKYIVSASGDRTIKWSTS 391			
Db 359 LMVTCSDRSIAVWDMASPTDTLRRVLYGHRRAAVNVDFDDKYIVSASGDRTIKWSTS 418			

Qy 392 TCEFVRTLNGHKGIACLQYDRDLVUVSSSDNTIRLWIECGACLRVLEGHEBLVRCRF 451
 Db 419 TCEFVRTLNGHKGIACLQYDRDLVUVSSSDNTIRLWIECGACLRVLEGHEBLVRCRF 478
 Qy 452 DNKRIVSGAYDGKIKWMDQALDPRAPASTLCLRTLYEHSGRVFRLOFDEFQIISSSH 511
 Db 479 DNKRIVSGAYDGKIKWMDQALDPRAPASTLCLRTLYEHSGRVFRLOFDEFQIISSSH 538
 Qy 512 DTILWDFLNVPSPQAQNTRSPSRTRYISR 542
 Db 539 DTILWDFLNDPAAQAEPPRSPSRTRYISR 569

RESULT 8

US-10-632-150-2
 Sequence 2, Application US/10632150
 Publication No. US20050251871A1
 GENERAL INFORMATION:
 APPLICANT: Chiaur, D.
 APPLICANT: Latres, E.
 APPLICANT: Pagano, M.
 TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
 CURRENT APPLICATION NUMBER: US/10/632,150
 CURRENT FILING DATE: 2003-07-30
 PRIOR APPLICATION NUMBER: 60/09/385, 219
 PRIOR FILING DATE: 1999-08-27
 PRIOR APPLICATION NUMBER: 60/098, 355
 PRIOR FILING DATE: 1998-08-28
 PRIOR APPLICATION NUMBER: 60/118, 568
 PRIOR FILING DATE: 1999-02-03
 PRIOR APPLICATION NUMBER: 60/124, 449
 PRIOR FILING DATE: 1999-03-15
 NUMBER OF SEQ ID NOS: 90
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 569
 TYPE: PCT
 ORGANISM: Homo sapiens

US-10-632-150-2

Query Match 82.8%; Score 2184.5; DB 5; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.3e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP----RSIWLGCANLV--ESMCAL 36
 Db 1 MDPAEAVLQEKAALKFMNSSEREDCNGGEPPKTIPKPEKNSLRQTYNSCARLCLNQETVCLA 60
 Qy 37 SCLQSMPSVRCL--QISNGTSSVIVSRKRPSSEGNYQEKDUCIKYFDQWSSESDQVEFVE 93
 Db 61 S--TAMKTCNTYAKTKELANGTSSMIVPKQKLSASYEKEKLVCKYFDQWSSESDQVEFVE 118
 Qy 94 HJISRMCHYQHGHNISYLPKMLQRFDTALPECGDLHTAENTLSYLDARSLSCLCAELYCKE 153
 Db 119 HJSQMCYQHGHNISYLPKMLQRFDTALPARGDLHTAENLTSYLDARSLSCLCAELYCKE 178
 Db 61 S--TAMKTCNTYAKTKELANGTSSMIVPKQKLSASYEKEKLVCKYFDQWSSESDQVEFVE 118
 Qy 94 HJISRMCHYQHGHNISYLPKMLQRFDTALPECGDLHTAENTLSYLDARSLSCLCAELYCKE 153
 Db 119 HJSQMCYQHGHNISYLPKMLQRFDTALPARGDLHTAENLTSYLDARSLSCLCAELYCKE 178
 Qy 154 WQVISSEGMLWKLLIERMVRTDPLWKGSERREGMDOYLFKNRPTDG--PPNSFYRSLYPK 211
 Db 179 WYRTSDGMWKLLIERMVRTDLSWRGLAERRGWQYLFKNRKPDPGNAPPNSFYRALYPK 238
 Qy 212 IIODIETESNWRGRHLNQRIQRSSENSKGYCLQYDEKAIISGLRLRSKIKWDKTSLE 271
 Db 239 IIODIETESNWRGRHLNQRIQRSSENSKGYCLQYDEKAIISGLRLRSKIKWDKTSLE 298
 Qy 272 CLKVLTGHGTSVLCLOYDERVITYGSSPSTVRYWDNTGEVNTLHNEAVLHRLFNG 331
 Db 299 CKRLTGHTGSVLCLOYDERVITYGSSPSTVRYWDNTGEVNTLHNEAVLHRLFNG 358
 Qy 332 LMTCSKRSIAWDMASATDITLRRVLYGHRAAVNTDFDDKIVTSSGDRTIKWSTS 391
 Db 359 MNVTCSKRSIAWDMASPTDITLRRVLYGHRAAVNTDFDDKIVTSSGDRTIKWSTS 418
 Qy 392 TCEFVRTLNGHKGIACLQYDRDLVUVSSSDNTIRLWIECGACLRVLEGHEBLVRCRF 451
 Db 419 TCEFVRTLNGHKGIACLQYDRDLVUVSSSDNTIRLWIECGACLRVLEGHEBLVRCRF 478
 Qy 452 DNKRIVSGAYDGKIKWMDQALDPRAPASTLCLRTLYEHSGRVFRLOFDEFQIISSSH 511
 Db 479 DNKRIVSGAYDGKIKWMDQALDPRAPASTLCLRTLYEHSGRVFRLOFDEFQIISSSH 538

RESULT 1.0

US-11-073-470-2

Sequence 2, Application US/11073470

GENERAL INFORMATION:

APPLICANT: PAGANO, M.

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS

FILE REFERENCE: 5914-090-999

CURRENT APPLICATION NUMBER: US/11/073,470

CURRENT FILING DATE: 2005-03-04

PRIOR APPLICATION NUMBER: 10/042,417

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: 60/260,179

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 92

SEQ ID NO: 2

TYPE: PRT

ORGANISM: Homo sapiens

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 2

LENGTH: 569

Query Match 82.8%; Score 2384.5; DB 6; Length 569;

Best Local Similarity 79.0%; Pred. No. 5.3e-201;

Matches 451; Conservative 48; Mismatches 41; Gaps 7;

Query 1 MEP-DSVIDTIELMCS-----VP---RSIWLGCANLV--ESMCAL 36

Db 1 MDPAEAVLOEKALKFMNSSEREDCNNGEPRKIIPEKNSTQYNTSCARCLNQETVCA 60

Query 37 SCLQSMPSVRCL--QISNGTSSYTVRGPSEGNYQEKDLCKYFDWSESQVEFE 93

Db 61 S--TAMKTENCVAKTKLANGTSSMIVPKQRLSASYEKEKLCKYFDWSESQVEFE 118

Query 94 HLISRMCHYQGHINSYLKPMQLORDFTALPQEGDHAENILSYDLARSCLCAELYCKE 153

Db 119 HLISQMCHYQGHINSYLKPMQLORDFTALPARGLDHAENILSYDLARSCLCAELYCKE 178

Query 61 S--TANKTENCVAKTKLANGTSSMIVPKQRLSASYEKEKLCKYFDWSESQVEFE 118

Query 94 HLISRMCHYQGHINSYLKPMQLORDFTALPQEGDHAENILSYDLARSCLCAELYCKE 153

Db 119 HLISQMCHYQGHINSYLKPMQLORDFTALPARGLDHAENILSYDLARSCLCAELYCKE 178

Query 154 WQRYISSEGMLWKLLIERNVRTDPLWKGJLSERGWDQYLFKNRPTDGG--PPNSPYRSLYPK 211

Db 179 WYRTSDGMWKLLIERNVRTDLSLRGLAERRGWQYLFKNPKGDNAPPNSPYRSLYPK 238

Query 212 IIOQDIEIESNWRCGRHNLRQRIQRSENSKGYCLQYDDEKISGLRONSISKWDKTSLE 271

Db 239 IIOQDIEIESNWRCGRHNLRQRIQRSENSKGYCLQYDDEKISGLRONSISKWDKNTLE 298

Query 272 CLKVLTGHTGSVLCLQYDERRIVTGSSDSTVRDVNTGEVNLTLHNEAVLHLRFNSG 331

Db 359 MMVTKSOKRSIAWTDMASPTDITIRVLRVGHRAAVNVYDDKXYVASGDRTKWNNTS 418

Query 392 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKTSLE 271

Db 299 CKRLTGHTGSVLCLQYDERRIVTGSSDSTVRDVNTGEVNLTLHNEAVLHLRFNSG 358

Query 332 LMVTKSOKRSIAWTDMASATDITIRVLYGHRAAVNVYDDKXYVASGDRTKWNNTS 391

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 272 CLKVLTGHTGSVLCLQYDERRIVTGSSDSTVRDVNTGEVNLTLHNEAVLHLRFNSG 331

Db 359 MMVTKSOKRSIAWTDMASPTDITIRVLRVGHRAAVNVYDDKXYVASGDRTKWNNTS 418

Query 332 LMVTKSOKRSIAWTDMASATDITIRVLYGHRAAVNVYDDKXYVASGDRTKWNNTS 391

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 272 CLKVLTGHTGSVLCLQYDERRIVTGSSDSTVRDVNTGEVNLTLHNEAVLHLRFNSG 331

Db 359 MMVTKSOKRSIAWTDMASPTDITIRVLRVGHRAAVNVYDDKXYVASGDRTKWNNTS 418

Query 392 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKTSLE 271

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 332 LMVTKSOKRSIAWTDMASATDITIRVLYGHRAAVNVYDDKXYVASGDRTKWNNTS 391

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 359 MMVTKSOKRSIAWTDMASPTDITIRVLRVGHRAAVNVYDDKXYVASGDRTKWNNTS 418

Query 392 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKTSLE 271

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 332 LMVTKSOKRSIAWTDMASATDITIRVLYGHRAAVNVYDDKXYVASGDRTKWNNTS 391

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 359 MMVTKSOKRSIAWTDMASPTDITIRVLRVGHRAAVNVYDDKXYVASGDRTKWNNTS 418

Query 392 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKTSLE 271

Db 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 419 TCEFVRTLNGHKGRTGIACLQYDDEKISGLRONSISKWDKNTLE 478

Query 452 DNKRIVSGAYDGKIKWDLQAOALDPRAPASTLCLRTLVHSGRYVRLOQDEFQISSLHD 511

Db 479 DNKRIVSGAYDGKIKWDLVAALDPRAPAGTLCLRTLVHSGRYVRLOQDEFQISSLHD 538

Query 512 DTILIWFELNDPAQAQPSPRSRTTYISR 542

Db 539 DTILIWFELNDPAQAQPSPRSRTTYISR 569

Query 512 DTILIWFELNDPAQAQPSPRSRTTYISR 542

Db 539 DTILIWFELNDPAQAQPSPRSRTTYISR 569

Query 512 DTILIWFELNDPAQAQPSPRSRTTYISR 542

Db 539 DTILIWFELNDPAQAQPSPRSRTTYISR 569

RESULT 1.2

US-11-094-691-12

Sequence 12, Application US/11099691
 GENERAL INFORMATION:
 APPLICANT: INCYTE PHARMACEUTICALS, INC.
 APPLICANT: BANDMAN, Olga
 APPLICANT: HILLMAN, Jennifer L.
 APPLICANT: LAL, Preeti
 APPLICANT: YOB, Henry
 APPLICANT: TANG, Y. Tom
 APPLICANT: PATTERSON, Chandra
 APPLICANT: BAUGHN, Marlia R.
 APPLICANT: YANG, Junming
 TITLE OF INVENTION: CELL SIGNALING PROTEINS
 CURRENT APPLICATION NUMBER: US/11/099,691
 CURRENT FILING DATE: 2005-04-06
 PRIOR APPLICATION NUMBER: US/09/700,444
 PRIOR FILING DATE: 2002-08-26
 PRIOR APPLICATION NUMBER: 60/085,343
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/098,010
 PRIOR FILING DATE: 1998-08-26
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PERL Program
 SEQ ID NO: 12
 LENGTH: 569
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc-feature
 OTHER INFORMATION: Incyte Clone 3239149
 US-11-099-691-12

Query Match 82.8%; Score 2384.5; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 5.e-201;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSIWLGCANLV--ESMCAL 36
 Db 1 MDPAEAVLQEALKFPMNSSEREDCNGGPPRKIPEKNSLRQTYNSCARLNQETVCLA 60

Qy 1 MEP-DSVIEDKTIELMCS-----VP-----RSIWLGCANLV--ESMCAL 36
 Db 1 MDPAEAVLQEALKFPMNSSEREDCNGGPPRKIPEKNSLRQTYNSCARLNQETVCLA 60

Qy 37 SCLOSMPSVRCL---QISNGTSSYIVSRPSEGNYQEKDLCIKYFDQWSSESDQVEFE 93
 Db 61 S---TAMKTCENCVAKTKLANTGTSIVPKQKLASAYEEKEKELCKYFQWSSESDQVEFE 118

Qy 94 HLISRMCHYQHGHSYKPLQDFITALPEQGLDHIAENILSYLDARSILCAELYCKE 153
 Db 119 HLISQMCHYQHGHSYKPLQDFITALPARGLDHIAENILSYLDARSILCAELYCKE 178

Qy 154 WQRVISEGMLWKLIERMVRTDPLWKGSERGRWDQYIFKNRPDTG--PPNSPYRSLYPK 211
 Db 179 WWRVTSDMWLWKLIERMVRTDPLWKGSERGRWDQYIFKNRPDTG--PPNSPYRSLYPK 238

Qy 212 IQDIEITESNWRCGHNLQRIQCRSENKGYCYLOQDDEKITSGLRDNSTIKIWDKTSLE 271
 Db 239 IQDIEITESNWRCGHNLQRIQCRSENKGYCYLOQDDEKITSGLRDNSTIKIWDKTSLE 271

Qy 272 CLKVLTGHTGSVLCLQYDERVITGSSSTVRYDNTGEVNTLHNEAHLRLRFNG 331
 Db 299 CKRLTGHTGSVLCLQYDERVITGSSSTVRYDNTGEVNTLHNEAHLRLRFNG 358

Qy 332 LMVTCSDRSIAWDMASATDITLRRVLYGHRAAVNVDDKYIVSASGDRTIKWSTS 391
 Db 359 MMVTCSDRSIAWDMASPTDITLRRVLYGHRAAVNVDDKYIVSASGDRTIKWSTS 418

Qy 392 TCFEVRTLNGHKRGIACLQYDRLLVSGSSDNTIRLWIEGACLRVLEGHEELVRCLR 451
 Db 419 TCFEVRTLNGHKRGIACLQYDRLLVSGSSDNTIRLWIEGACLRVLEGHEELVRCLR 478

Qy 452 DNKRIVSGAYDGKIKWDLQAAIDPRAASTICLRTLVEHSGRVFRQDEFQISSLSD 511
 Qy 479 DNKRIVSGAYDGKIKWDLVAALDPRAPGTCLRTLVEHSGRVFRQDEFQIVSSSD 538

Qy 512 DTIWIWFLNPSSAQNETRSPRTYYSR 542
 Db 539 DTIWIWFLNDPAAQAEPFRSPRTYYSR 569

RESULT 14
US-10-687-732-18
Sequence 18, Application US/10687732
Publication No. US20040171074A1
GENERAL INFORMATION:
APPLICANT: Orlicky, Stephen
APPLICANT: Sicheri, Frank
APPLICANT: Tyers, Mike
APPLICANT: Willems, Andrew
APPLICANT: Tang, Xiaojing
TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
FILE REFERENCE: 14096_34USU1
CURRENT APPLICATION NUMBER: US/10/687,732
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/419,606
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 569
TYPE: PRT
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/NP_033901
DATABASE ENTRY DATE: 1998-08-04
RELEVANT RESIDUES: (1) ... (569)
US-10-687-732-18

Query Match Score 82.5%; Best Local Similarity 78.8%; Pred. No. 3.3e-200; Matches 449; Conservative 49; Mismatches 42; Indels 31; Gaps 7;

Db 1 MEPAEAVLQEALKFMSKSERDNCNGEPPRKPIPEKNSLRQTYNSCARLCINOETVCLT 36
Db 1 MDPAEAVLQEALKFMSKSERDNCNGEPPRKPIPEKNSLRQTYNSCARLCINOETVCLT 60

Query 37 SCIQSMPSVRCL--Q1SNGTSSVYTSRKRPSSEGNYQEKDLCKYKFDMSESDOVEFVE 93
6 1 S-TAMKTEVYAKAKLNGTSMIVPKQLKUSASTERKEELCVKLQFQNSESDOVEFVE 118
Db 94 HLIJSMCHYQHGHINSYKPMQLQDFITALPROGLDHIAENILSYLDARSILCAAEVLCKE 153
Db 119 HLIJSMCHYQHGHINSYKPMQLQDFITALPARGLHDIAENILSYLDASKCAEVLCKE 178

Query 154 WQVISEBMLWKLIEENVTDPLWKGLSERGWQDQLFLKRPPTD--GPNSFIRSLYPK 211
Db 179 WYRVTSQGMLWKLIEENVTDPLWKGLSERGWQDQLFLKRPPTD--GPNSFIRSLYPK 238

Query 212 IIQDIETTESWRGCRGRNLIORIQCRESNSKGYYCLOYDDEKIIISGRDNISKIWDTKSL 271
Db 239 IIQDIETTESWRGCRGRNLIORIQCRESNSKGYYCLOYDDEKIIISGRDNISKIWDTKSL 298

Query 272 CLKVLTGHTGSVLCLOYDERVITVGSSSDTWRWDNTGEVNLTLIHNEAVLHLRFNSG 331
Db 299 CKRLTGHTGSVLCLOYDERVITVGSSSDTWRWDNTGEVNLTLIHCEAVLHLRFNSG 358

Query 322 LAVTCRSKRSIAWDMASATDITLRRVYHGAAVNTUDFDKTYISASGRTIKWTS 391
Db 359 MMVTCRSKRSIAWDMASPTDITLRRVYHGAAVNTUDFDKTYISASGRTIKWNT 418

Query 392 TCFEFVRTLNGHKGIACLQYDRLVWSGSSDNTIRLMDIECGACLRYLEGHPELVRCAF 451
Db 419 TCFEFVRTLNGHKGIACLQYDRLVWSGSSDNTIRLMDIECGACLRYLEGHPELVRCAF 478

Query 452 DNKRIVSGAYDGKIKVNDLQALDPRAPASTLCLRTLVEHSGRVFLQDFEQLISSHD 511
Db 479 DNKRIVSGAYDGKIKVNDLQALDPRAPASTLCLRTLVEHSGRVFLQDFEQLISSHD 538

Query 512 DTILIWDDLNVPSSAQNTRSPTRTYIISR 542
Db 539 DTILIWDDLNVPSSAQNTRSPTRTYIISR 569

RESULT 15
US-11-097-143-6363
Sequence 6363, Application US/11097143
Publication No. US2005020558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,131
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 4308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6163
LENGTH: 510
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-6363

Query Match Score 2077.5%; Best Local Similarity 80.8%; Pred. No. 5.2e-174; Matches 384; Conservative 44; Mi.matches 46; Indels 1; Gaps 1;

Db 61 RKRPPSEGNQYQEKDLCKYKFDPWSSESDOVEFVEHLISRMCHYQHGHINSYLKPMQLORDFI 120
Db 30 RKKDQSPPTCYOTERELCFQYFTQWSQSVQDVEFHLSRMCHYQHGOINAYLKPMQLORDFI 89

Query 61 TALPEGOLDHIAENILSYLDARSILCAEVLCKEWNRVISEGMLWKLIEENVTDPLWKG 180
Db 90 TLLPKGLDHAENILSYLDAESLKSSELVCKEWNRVISEGMLWKLIEENVTDPLWKRG 149

Query 181 LSERGRGDQYLFKNRPTDGP--PNSYPSRLYPKIIDIETTESWRGCRGRNLIORIQCRESN 239
Db 150 LAERRWQMQLIFKPRLGQTQPHSPHRELFKIMNDIDS1ENNWTGRHMLRRINCSEN 209

Query 240 SKGVYCLQYDDEKIIISGRDNISKIWDTKSLECLVKLTGHTGSVLCLOYDERVITVGSSD 299
Db 210 SKGVYCLQYDQGKIVSGLRDNITKWDRTDLCQVTKLGMHTGSVLCLOYDKVTKVIGSSD 269

Query 300 STVRWDVNTCEVNLTLIHNEAVLHLRFNSGMLMTCRSKRSIAWDMASATDITLRRV 359
Db 270 STVRWDVNTGEMVNTLICHCEAVLHLRFNSGMLMTCRSKRSIAWDMTSSEITLRRV 329

Query 360 VGHRAAVNVVDQDDKYIVSAGGDRITKWKSTSTCEFVRTLNGHKGIACLQYDRLVSG 419
Db 330 VGHRAAVNVVDEDEKIVTASGDRITKWKSTSCFVRTLNGHKGIACLQYDRLVSG 389

Query 420 SSDNTIRLWDIECGACLRLVEGHEELVRCIRFDNKRIVSGAYDGKIKVNDLQALDPRAP 479
Db 390 SSDNSIRLWDIECGACLRLVEGHEELVRCIRFDNKRIVSGAYDGKIKVNDLVAALDRAA 449

Query 480 ASTLCLRTLVEHSGRVFLQDEFQIISSHDDTLLIWFNFVPPSAQNERTRSPS 534
Db 450 SNTLCLNTLVEHSGRVFLQDEFQIVSSSHDDTLLIWFNFVPPSAQNERTRSPS 504

Search completed: August 25, 2006, 07:38:23
Job time : 187 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	2879	100.0	542	6 US-10-965-871-6	Sequence 6, App1
2	2384.5	82.8	569	6 US-10-968-871-3	Sequence 3, App1
3	2384.5	82.8	569	7 US-11-106-014-2	Sequence 2, App1
4	416.5	14.5	1281	6 US-10-441-902-42332	Sequence 42332, A
5	329.5	13.7	415	7 US-11-293-697-4324	Sequence 4324, AD
6	329.5	11.4	317	7 US-11-056-355B-90488	Sequence 90488, A
7	329.5	11.4	317	7 US-11-056-355B-94244	Sequence 94244, A
8	327.5	11.4	422	7 US-11-106-014-4	Sequence 4, App1
9	326	11.3	891	6 US-10-449-902-54504	Sequence 54504, A
10	323	11.2	267	7 US-11-056-355B-37531	Sequence 37531, A
11	323	11.2	267	7 US-11-056-355B-85524	Sequence 85524, A
12	323	11.2	333	7 US-11-056-355B-37530	Sequence 37530, A
13	323	11.2	333	7 US-11-056-355B-85523	Sequence 85523, A
14	323	11.2	654	6 US-10-449-902-50780	Sequence 50780, A
15	318.5	11.1	808	6 US-10-449-902-41350	Sequence 41350, A
16	308.5	10.7	319	7 US-11-056-355B-13037	Sequence 13037, A
17	308.5	10.7	346	7 US-11-056-355B-13036	Sequence 13036, A
18	299.5	10.2	1194	7 US-11-045-540-2	Sequence 2, App1
19	292.5	10.2	1205	7 US-11-045-540-3	Sequence 3, App1
20	289	10.0	324	6 US-10-449-902-36608	Sequence 36608, A
21	286.5	10.0	326	7 US-11-056-355B-26636	Sequence 26636, A
22	286.5	10.0	326	7 US-11-056-355B-38851	Sequence 38851, A
23	284.5	10.0	326	7 US-11-056-355B-86112	Sequence 86112, A
24	284.5	9.9	326	7 US-11-056-355B-24773	Sequence 24773, A
25	283.5	9.8	311	6 US-10-951-349-37148	Sequence 37148, A

Qy 361 GHRAAYNVDDDKYIVTVAASGDRTIKVWSTSTCEVRTLNGKRGIACTQYRDLVVSGS 420
 Db 361 GHRAAYNVDDDKYIVTVAASGDRTIKVWSTSTCEVRTLNGKRGIACTQYRDLVVSGS 420

Qy 421 SDNTIRLWDIEGACLRVLSHEELVRCTIRDPKRIVSGAYDGKIKWDLQAALDPRPA 480
 Db 421 SDNTIRLWDIEGACLRVLSHEELVRCTIRDPKRIVSGAYDGKIKWDLQAALDPRPA 480

Qy 481 STLCRTLVEISGRVFLQFDEQIISSHDDTILWDFLNVPPEAQNETRSPSRTYI 540
 Db 481 STLCRTLVEISGRVFLQFDEQIISSHDDTILWDFLNVPPEAQNETRSPSRTYI 540

Qy 541 SR 542
 Db 541 SR 542

RESULT 2
 US-10-968-871-3
 ; Sequence 3, Application US/10968871
 ; Publication No. US20060177839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: New York University
 ; TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to
 ; TITLE OF INVENTION: DNA Damage
 ; FILE REFERENCE: 05986/0200145-US0
 ; CURRENT APPLICATION NUMBER: US/10/968,871
 ; CURRENT FILING DATE: 2004-10-18
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-968-871-3

Query Match 82.8%; Score 2384; DB 6; Length 569;
 Best Local Similarity 79.0%; Pred. No. 2e-184;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP----RSIWCANLY--ESMCAL 36
 Db 1 MDPAEAVLQEALKFENNSSEREDCNNGEPKRKIPPEKNSLRQTNNSCARCLNQETVCLA 60

Query Match 82.8%; Score 2384; DB 7; Length 569;
 Best Local Similarity 79.0%; Pred. No. 2e-184;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 37 SCLQSMPSVRCL---QISNGTSSVIVSRKRPSGEQYQEKDLCIYFQDWSSEDOVEFVE 93
 Db 61 S---TANKTENCVAKTKLNGTSSMTPVKQLSLASYTEKELCVKYFQDWSSEDOVEFVE 118

Qy 94 HLISRMCHYQHGHNSVYLPMLKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 211
 Db 119 HLISQMCHYQHGHNSVYLPMLKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 178

Qy 154 WORVISGMLWKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 211
 Db 179 WYRVTSGMLWKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 238

Qy 212 IIQDIEITESWRGRHLNQLQRCSSENISGVYCLQYDDEKLISGRDNTIKIWDTKTSLE 271
 Db 239 IIQDIEITESWRGRHLNQLQRCSSENISGVYCLQYDDEKLISGRDNTIKIWDTKNTLE 298

Qy 272 CLKVLTSHTGSVLCLOYDERVITVGSSDSTVRMDVNTGEVNLTHHNEAVLHLRFNSG 331
 Db 299 CKRLTGTGSVLCLOYDERVITVGSSDSTVRMDVNTGEVNLTHHNEAVLHLRFNSG 358

Qy 332 LMVTCSKDRSIAWDMASATDITLRLVYLGHRRAAVNVVDFFDKYIVTVAASGDRTIKWSRS 391
 Db 359 MNVTCSKDRSLAWDMASPTDITLRLVYLGHRRAAVNVVDFFDKYIVTVAASGDRTIKWNTS 418

Qy 392 TCFEVTRLNGKRGIACTQYRDLVVSGSDNTIRLWIEGACLRVLEGHEELVRCIRF 451
 Db 419 TCFEVTRLNGKRGIACTQYRDLVVSGSDNTIRLWIEGACLRVLEGHEELVRCIRF 478

Qy 452 DNKRIVSGAYDGKIKWDLQAALDPRAPASTLCLRVLVEHSGRVFLQFDEFOLISSHD 511
 Db 479 DNKRIVSGAYDGKIKWDLQAALDPRAPACTLCLRVLVEHSGRVFLQFDEFOLISSHD 538

Qy 512 DTLLWDFLNVPPEAQNETRSPSRTYI 542
 Db 539 DTLLWDFLNPAQQAEPPRSPSRTYI 569

RESULT 3
 US-11-106-014-2
 ; Sequence 2, Application US/11106014
 ; Publication No. US20060088846A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pagano, Michele
 ; APPLICANT: Chlaar, Dah Sharim
 ; APPLICANT: Srivastava, Promod
 ; APPLICANT: Chandawarkar, Rajiv
 ; APPLICANT: Latres, Esther
 ; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
 ; FILE REFERENCE: 5914-106-999
 ; CURRENT APPLICATION NUMBER: US/11/106,014
 ; PRIORITY APPLICATION NUMBER: 10/1632,150
 ; PRIOR FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: 10/042,417
 ; PRIOR FILING DATE: 2002-01-07
 ; PRIOR APPLICATION NUMBER: 09/385,219
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: 60/118,566
 ; PRIOR FILING DATE: 1999-02-03
 ; PRIOR APPLICATION NUMBER: 60/098,355
 ; PRIOR FILING DATE: 1998-08-28
 ; PRIOR APPLICATION NUMBER: 60/124,449
 ; PRIOR FILING DATE: 1997-03-15
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 569
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-106-014-2

Query Match 82.8%; Score 2384; DB 7; Length 569;
 Best Local Similarity 79.0%; Pred. No. 2e-184;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MEP-DSVIEDKTIELMCS-----VP----RSIWCANLY--ESMCAL 36
 Db 1 MDPAEAVLQEALKFENNSSEREDCNNGEPKRKIPPEKNSLRQTNNSCARCLNQETVCLA 60

Qy 37 SCLOQNPSPVRLC---QISNGTSSVIVSRKRPSGEQYQEKDLCIYFQDWSSEDOVEFVE 93
 Db 61 S---TANKTENCVAKTKLNGTSSMTPVKQLSLASYTEKELCVKYFQDWSSEDOVEFVE 118

Qy 94 HLISRMCHYQHGHNSVYLPMLKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 211
 Db 119 HLISQMCHYQHGHNSVYLPMLKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 178

Qy 154 WQRVSEGMLWKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 211
 Db 179 WYRVTSGMLWKKLIERMVRDPLWKGLSERGRWQYLFKNRPTDG-PPNFSYSLYPK 238

Qy 212 IIQDIEITESWRGRHLNQLQRCSSENISGVYCLQYDDEKLISGRDNTIKIWDTKTSLE 271
 Db 239 IIQDIEITESWRGRHLNQLQRCSSENISGVYCLQYDDEKLISGRDNTIKIWDTKNTLE 298

Qy 272 CLKVLTSHTGSVLCLOYDERVITVGSSDSTVRMDVNTGEVNLTHHNEAVLHLRFNSG 331
 Db 299 CKRLTGTGSVLCLOYDERVITVGSSDSTVRMDVNTGEVNLTHHNEAVLHLRFNSG 358

Qy 332 LMVTCSKDRSIAWDMASATDITLRLVYLGHRRAAVNVVDFFDKYIVTVAASGDRTIKWSRS 391
 Db 359 MNVTCSKDRSLAWDMASPTDITLRLVYLGHRRAAVNVVDFFDKYIVTVAASGDRTIKWNTS 418

Qy 392 TCFEVTRLNGKRGIACTQYRDLVVSGSDNTIRLWIEGACLRVLEGHEELVRCIRF 451
 Db 419 TCFEVTRLNGKRGIACTQYRDLVVSGSDNTIRLWIEGACLRVLEGHEELVRCIRF 478

Qy 452 LMVTCSKDRSTAVWDMASTADITLRLVYLGHRRAAVNVVDFFDKYIVTVAASGDRTIKWNSTS 391

FILE REFERENCE: H1-A0106 ;
 CURRENT FILING DATE: 2005-12-05 ;
 PRIORITY APPLICATION NUMBER: US/10/108,260 ;
 PRIORITY FILING DATE: 2002-01-28 ;
 NUMBER OF SEQ ID NOS: 5458 ;
 SOFTWARE: PatentIn Ver. 2.1 ;
 SEQ ID NO: 2124 ;
 TYPE: PRT ;
 ORGANISM: Homo sapiens ;
 US-11-293-697-4324

Query Match Score 395; DB 7; Length 415;
 Best Local Similarity 25.8%; Pred. No. 4.5e-24;
 Matches 103; Conservative 79; Mismatches 140; Indels 78; Gaps 15;

RESULT 4
 US-10-449-902-42332 ;
 Sequence 42332, Application US/10449902 ;
 Publication No. US20060123505A1 ;
 GENERAL INFORMATION ;
 APPLICANT: National Institute of Agrobiological Sciences .
 Bio-oriented Technology Research Advancement Institution .
 The Institute of Physical and Chemical Research .
 Foundation for Advancement of International Science .
 TITLE OF INVENTION: FULL LENGTH PLANT CDNA AND USES THEREOF .
 FILE REFERENCE: MOA-A203Y1-US
 CURRENT APPLICATION NUMBER: US/10/449,902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-183870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 42332
 LENGTH: 1281
 TYPE: PRT
 ORGANISM: Oryza sativa
 US-10-449-902-42332

Query Match Score 416.5; DB 6; Length 1281;
 Best Local Similarity 35.8%; Pred. No. 3.8e-25;
 Matches 105; Conservative 49; Mismatches 104; Indels 35; Gaps 9;

RESULT 5
 US-11-293-697-4324 ;
 Sequence 4324, Application US/11293697 ;
 Publication No. US2006010376A1 ;
 GENERAL INFORMATION ;
 APPLICANT: HELIX RESEARCH INSTITUTE ;
 TITLE OF INVENTION: Nova null length cDNA

Query Match Score 329.5; DB 7; Length 317;
 Best Local Similarity 31.0%; Pred. No. 6.1e-19;
 Matches 111; Conservative 71; Mismatches 100; Indels 102; Gaps 10;

RESULT 8
US-11-106-014-4
; Sequence 4, Application US/1106014
; Publication No. US/1106014
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiaro, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; CHANDAWARKER, Raviv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; TITLE OF INVENTION: OF INVENTION: FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106, 014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-4

RESULT 7
US-11-056-35B-94244
; Sequence 94244, Application US/1105635B
; GENERAL INFORMATION:
; PUBLICATION NO. US200615023A1
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrova, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 275-0-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,3553
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 94244
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(317)
; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-35B-94244

Query Match 11.4%; Score 329.5; DB 7; Length 317;
Best Local Similarity 31.0%; Pred. No. 6.1e-19; Gaps 7;

Matches 76; Conservative 50; Mismatches 102; Indels 17; Gaps 7;

Qy 238 ENSKGVYCLQYDDEKISGLRDNSTIKIWDTKSLECLKVLTGHTGSVLCLOYD--ERVTWT 295
Db 71 ENGSDVAFSSDARFIVASDDDKTLLWVBTGSLIKTLIGHTNIAFCVNPNQSNMIVS 130

Qy 296 GSSDSTRVWDNTNGEVLTNLHNAVLHRSF--NGLMUTCSKDRSIAWDMASATDI 353
Db 131 GSFDETTRIWDTGCKLKVPAHSIDPVTAVDNRDGSIVSSYDGLCRWID--SGTGH 188

Qy 354 TLRRLVGHRAAVNWDF--DDKIVTYSASGDTIKWSTTCFVRTLGHKGIACLQ- 410
Db 189 CVKLIDDENPPVSFVRSPNGKFIVLGTDNTLRLWNISSAKFLKTYTGHVNAQYCLIS 248

Qy 411 ---YRDRLVYGSSEDNCVHMELNSKLLQKLEGTEVMVACHPTEN-LIASGSLDK 307
Db 249 AFSVTINGKRIVSGSEDNCVHMELNSKLLQKLEGTEVMVACHPTEN-LIASGSLDK 307

Qy 464 KIKW 468
Db 308 TVRIW 312

US-10-449-902-54504
 ; Sequence 54504, Application US/10449902
 ; Publication No. US2006012350A1
 ; GENERAL INFORMATION
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOR-A0205Y1-US
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIORITY FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54504
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-54504

Query Match 11.3%; Score 326; DB 6; Length 891;
 Best Local Similarity 27.4%; Pred. No. 4.7e-18;
 Matches 80; Conservative 61; Mismatches 119; Indels 32; Gaps 9;
 Query 249 DDEKTISSLRDNNSIKWIKDTSLECLVKIQLTGHITVCL-----QYDRIVTGTSSDSTVR 303
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12680898
 ; US-11-056-355B-85524

RESULT 10
 US-11-056-155B-37531
 ; Sequence 37531, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 37531
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 223 WRCGRHLNLRQCRSENSKGVYCLQY--DDEKTISSLRDNNSIKWIKD-KTSLECLVKIQLTGH 279
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12680898
 ; US-11-056-355B-85524

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 223 WRCGRHLNLRQCRSENSKGVYCLQY--DDEKTISSLRDNNSIKWIKD-KTSLECLVKIQLTGH 279
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 280 TGSVLCLQYD--ERIVTGSSDSTVRWDNTGEVNLTHNEAV--LHLRFSGHMT 335
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 336 CSKDRTSAVWDMASADITLRLVPHRAAVNNVDF--DDKVISSASGDRITKWKSTSTC 393
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 394 EFVRTLNGHKRGIACLQ----YRDLRVVSGSSDNTIRLWIECGACLRVLEGHEEL-- 445
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Query Match 11.2%; Score 323; DB 7; Length 267;
 Best Local Similarity 30.6%; Pred. No. 1.6e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;
 Query 446 VRCIRFDNKRKIVSGAY-DGKIKWMDLQA 472
 ; Sequence 85524, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nikolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE OF INVENTION: Polypeptides Encoded Thereby
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIORITY FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 85524
 ; LENGTH: 267
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE: peptide
 ; LOCATION: (1).:(267)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12335591
 ; US-11-056-355B-37531

Db 240 VSCHPVQNEISSSGNHLDDKTRIKWQDA 267
 RESULT 12
 US-11-056-355B-37530
 ; Sequence 37530, Application US/11056355B
 ; Publication No. US2006150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-15900US2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO: 37530
 ; LENGTH: 333
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide_id
 ; LOCATION: (1)..(333)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12680897
 ; US-11-056-355B-85523

Query Match 11.2%; Score 323; DB 7; Length 333;
 Best Local Similarity 30.6%; Pred. No. 2..2e-18;
 Matches 82; Conservative 55; Mismatches 109; Indels 22; Gaps 10;

Qy 223 WRCGRHNLRQCRSENKGVYCLQY--DDEK1ISGLRDNNSIKWD-KTSLECKVLGKTH 279
 Db 70 WSATNYSL-IRHYEGHSSGKSLAWSSDHYTCSASDCTLRIWDAKSPYECIKVLRGH 127

Qy 280 TGSVLCIQLQYD--ERVIVTGSSDSTVRWDNTGEVLNLTIHNEAV--LHLRFSGNLWYT 335
 Db 128 TNFVFVNFPNPSNLIVSGSFDETRIVEVKTCVRMKAHSMPISSFHENDGSLIVS 187

Qy 336 CSKDRSIAYNDMASATDTIIRRVLGHRAAVNVVF--DDKYIVSASGDRTIKWSTSTC 393
 Db 188 ASHDGSKLWDKDAEKGTT-CLKTLDKSPAVSPAKSPNGKFILATLDSLKLNSNYATG 245

Qy 394 EFTVTLNGHKGIACLQ---YRDLRVSGSSDNTIRLWDIEGGACRVLLEGHEEL-- 445
 Db 246 KFLKVYTGHTNKVFCTSAFSVTNCKYIVSGSEDCVYLWDLQARNILQRLEGHTDAVIS 305

Qy 446 VRCIRFDNKRIVSGAY-DGKIKWDLQA 472
 Db 306 VSCHPVQNEISSSGNHLDDKTRIKWQDA 333

RESULT 14
 US-10-449-902-50780
 ; Sequence 50780, Application US/10449902
 ; Publication No. US2006013505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; APPLICANT: Foundation for Full-length Plant cDNA and USES THEREOF
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIORITY APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 50780
 ; LENGTH: 654
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-50780

Query Match 11.2%; Score 323; DB 6; Length 654;
 Best Local Similarity 25.9%; Pred. No. 5..5e-18;
 Matches 86; Conservative 55; Mismatches 103; Indels 88; Gaps 12;

Qy 242 GVYC-LOYDDEK1ISGLRDNNSIKWD-----KTS-----LE 271
 Db 338 GLNCSSISHDGLVGGFSDSSVWDMSKIGQPPTKTSQGENGLSQCERTSASDYGKR 397

Qy 272 CLKVLTGHKGVYCLQYDE--RVIVTGSSDSTVRWDNTGEVLNLTIHNEAVLHLRFs 329
 Db 398 PYTLEFGHSCPVSAFAESPGDFLIISSSDSTRIW-----STKUNAN----- 440

Qy 330 NGLMWTCSKDRSIAYNDMASATDTIIRRVLGHRAAVNVFDKQYIVSASGDRTIKWMS 389
 ; SEQ ID NO: 85523
 ; LENGTH: 333
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:

RESULT 13
 US-11-056-355B-85523
 ; Sequence 85523, Application US/11056355B
 ; Publication No. US2006150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-15900US2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO: 85523
 ; LENGTH: 333
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:

RESULT 15
 US-10-449-902-41350
 ; Sequence 41350, Application US/10449902
 ; Publication No. US2006012350A1

GENERAL INFORMATION:
 APPLICANT: National Institute of Agrobiological Sciences.
 Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205Y1.US

CURRENT APPLICATION NUMBER: US/10/449, 902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-383870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 41350
 LENGTH: 808
 TYPE: PRT
 ORGANISM: Oryza sativa
 US-10-449-902-41350

	Query Match	Score	Length
Qy	239 NSKGVVCLQYDDEKIKISGLRDNISKIKWDLTSDLE-----	318.5	808
Db	449 HSGTVKCLQVEDBVCITGTDHAIRIMDLTKVENFEARLSMTASGEILRKRSPLNRS 508	1.6e-17	6
Qy	272 -----CLKVLTGHGSVNLQYDVERIVYGS 298	64	271
Db	509 ELGDQSMDSIKIRDGDTPTVGEBDEEVVRGDFDCVKSLLEGHSKSITALYFDNNCLVTGAS 568	Mismatches	107
Qy	299 DSTVRVWDVNTGEVLNL-----	Indels	125
Db	569 DKTLRQWLNTSQCVLTMIDLWAISNPNTSSQAOISOSBGFPEPSRKAASSAILGSTRPE 628	Gaps	6
Qy	317 IHNNEAVIHLRFNSGLMWTCSKDRSLAWDMASATDITLRRVLGHRAYNVDFDDKYI 376	Matches	85
Db	629 LNSRDSFSVLNVNGAFAYPTPPYADGSWEM-----YQDFVGGVQFMGYAL 674	Conservative	64
Qy	377 VSASGDRTIKWMSTSTCEFVRTLNGHKRGIAQYRDRLVYGSQSDNTIRLWDIECGACL 436	-----	316
Db	675 ASGSGDGCVRMWDMRTCQAHRTLLGHTAPVTLQFDHVSGLDKSIRWLNGTSIS 734	-----	-----
Qy	437 RVLEGHEELVRCIREDNKRIVSGAYDGKIKWDLQAALDPAPASTLCLRLTVEHSGRVF 496	-----	785
Db	735 DTIR-YDHPVTAQFRKILAAATGEGVKIN-RTTLQHGA-----LTINGHTSPVE	-----	-----
Qy	497 RLQFDEQQISSHDDPTLIW 517	-----	-----
Db	786 RLRYMDTYAVGGKDSSVVKW 806	-----	-----

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